

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 18:46:24 ; Search time 19 seconds

(without alignments) 597.258 Million cell updates/sec

Title: US-09-898-860-2

Perfect score: 649

Sequence: 1 MPREDAHRTYGYPKKGHS.....NAPPAYEKLSAEQSPPPYSP 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	118	2 A55253	melanoma antigen M
2	87	13.4	4957	2 T03455	ALR protein - huma
3	87	13.4	5262	2 T03454	ALR protein - huma
4	80.5	12.4	344	2 B28967	T-cell surface gly
5	80.5	12.4	344	2 T49585	CD2 antigen protei
6	79	12.2	972	2 T49773	related to actin-I
7	77	11.9	710	2 E69665	nitrate reductase
8	73	11.2	1069	2 T00043	BH-protocadherin-a
9	72.5	11.2	1429	2 T13720	gene expanded prot
10	71.5	11.0	1265	2 T51314	probable CO- induce
11	71	10.9	1072	2 T00041	BH-protocadherin P
12	71	10.9	1200	2 T00042	BH-protocadherin P
13	70.5	10.9	254	2 H83334	probable transcrip
14	70	10.8	335	2 G88640	protein F52C12.3 f
15	70	10.8	346	2 H84512	hypothetical prote
16	70	10.8	2100	2 T03232	probable polyketid
17	69.5	10.7	341	2 T22633	hypothetical prote
18	69.5	10.7	404	2 H64175	hypothetical prote
19	69	10.6	940	2 E72100	fibronectin-bindin
20	68.5	10.6	384	2 E72100	hypothetical prote
21	68.5	10.6	476	2 T35769	probable transmem
22	68	10.5	316	2 C82085	conserved hypotet
23	68	10.5	377	2 C91270	beta-lactamase [im
24	68	10.5	377	2 C86111	beta-lactamase, pe
25	67.5	10.4	188	2 A64332	probable phosphono
26	67.5	10.4	315	2 T47971	seven in absentia-
27	67.5	10.4	476	2 T43464	hypothetical prote
28	67.5	10.4	670	2 T13739	probable hormone r
29	67.5	10.4	753	2 J00532	OP protein - Keene

30	67	10.3	485	2 S32171	hydroxyneurosporen
31	67	10.3	2723	2 T03221	probable polyketid
32	66.5	10.2	215	2 F71923	hypothetical prote
33	66	10.2	140	2 S67666	probable membrane
34	66	10.2	751	2 T31515	hypothetical prote
35	65.5	10.1	258	2 A48820	homeobox protein (
36	65.5	10.1	384	2 A86521	conserved hypotet
37	65.5	10.1	518	2 D69539	antigen WCL1 prec
38	65.5	10.1	1023	2 T46997	epsin-like protein
39	65.5	10.1	1436	2 A46496	hypothetical prote
40	65	10.0	309	1 E65112	hypothetical 34.6
41	65	10.0	309	2 B91140	hypothetical prote
42	65	10.0	309	2 E85985	conserved hypotet
43	65	10.0	309	2 AH0906	testicular hypotet
44	64.5	9.9	243	2 JEO204	fixz protein - Rhl
45	64.5	9.9	359	2 A22891	

ALIGNMENTS

RESULT 1
A55253
melanoma antigen MART-1 - human
N:Alternate names: melan-A protein
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 04-Mar-2000
C:Accession: A55253; I38506
R:Kawakami, Y.; Eliyahu, S.; Delgado, C.H.; Robbins, P.F.; Rivoltini, L.; Topalian
Proc. Natl. Acad. Sci. U.S.A. 91, 3515-3519, 1994
A>Title: Cloning of the gene coding for a shared human melanoma antigen recognized
A:Reference number: A55253; MUID:94224770; PMID:8170938
A:Accession: A55253
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <KAM>
A:Cross-references: GB:006452; NID:9476131; PIDN:AAA19238.1; PID:9476132
R:Conliffe, P.G.; Brichard, V.; Van Pel, A.; Wolfel, T.; Schneider, J.; Traversari, L.
J. Exp. Med. 180, 35-42, 1994
A>Title: A new gene coding for a differentiation antigen recognized by autologous
A:Reference number: I38506; MUID:94475389; PMID:8006593
A:Accession: I38506
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-118 <RES>
A:Cross-references: EMBL:U06654; NID:9517022; PIDN:AAA20389.1; PID:9517023
C:Genetics:
A:Gene: GDB:MLANA
A:Cross-references: GDB:358979
A:Map position: 17q21-17q24
C:Superfamily: human melanoma antigen MART-1

Query Match 100.0%; Score 649; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPREDAHRTYGYPKKGHSYTAEEAGIGLTYITLGVLLIGCYCRRRGYALMDK 60
DB 1 MPREDAHRTYGYPKKGHSYTAEEAGIGLTYITLGVLLIGCYCRRRGYALMDK 60
QY 61 SLHVGTCALTRRCPOEGFDHRDSKVSIOENKCEPVNAPPAYEKLSAEQSPPPYSP 118
DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSIOENKCEPVNAPPAYEKLSAEQSPPPYSP 118

RESULT 2

T03455
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03455
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.;
Oncogene 15, 549-560, 1997

A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4957 <PRA>
A:Cross-references: EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; PID:g2358287
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: human ALR protein
C:Keywords: alternative splicing

Query Match 13.4%; Score 87; DB 2; Length 4957;
Best Local Similarity 31.2%; Pred. No. 3.2;
Matches 25; Conservative 7; Mismatches 30; Indels 18; Gaps 3;

OY 41 LITGWCRRRNGRRLMDKSLHGTQCALTR---RCPOGPFDRDSKVSLOEKNCBPV 96
DB 939 LITGCRRCER-----WMHAGCESLFTEDVDVNAHPDGF-----CVSCQPYVVRV 984

OY 97 VPNAPEYKLSAQSPPY 116
DB 985 APVAPPELVPMKVEPEPOY 1004

RESULT 3
T03454
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03454
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03454
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5262 <PRA>
A:Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: human ALR protein
C:Keywords: alternative splicing

Query Match 13.4%; Score 87; DB 2; Length 5262;
Best Local Similarity 31.2%; Pred. No. 3.4;
Matches 25; Conservative 7; Mismatches 30; Indels 18; Gaps 3;

OY 41 LITGWCRRRNGRRLMDKSLHGTQCALTR---RCPOGPFDRDSKVSLOEKNCBPV 96
DB 1244 LITGCRRCER-----WMHAGCESLFTEDVDVNAHPDGF-----CVSCQPYVVRV 1289

OY 97 VPNAPEYKLSAQSPPY 116
DB 1290 APVAPPELVPMKVEPEPOY 1309

RESULT 4
B28967
T-cell surface glycoprotein CD2 precursor - mouse
N:Alternate names: CD2 antigen; T-lymphocyte antigen CD2; T11 protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1989 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: B28967; S01347; S02293
R:Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A:Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A:Reference number: A28967; MUID:88144486; PMID:2894031
A:Accession: B28967
A:Molecule type: mRNA

A:Residues: 1-344 <CD1A>
A:Cross-references: GB:M1807; NID:g192479; PIDN:AAA37393.1; PID:g387122; GB:J03622
A>Note: the authors translated the codon TAT for residue 99 as Thr
R:Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L.
Eur. J. Immunol. 17, 1367-1370, 1987
A:Title: Murine and human T11 (CD2) cDNA sequences suggest a common signal transduc
A:Reference number: S01347; MUID:88004738; PMID:2820751
A:Accession: S01347
A:Molecule type: mRNA
A:Residues: 1-127, 'M', 129-174, 'N', 176-190, 'NM', 193-344 <CD1A>
A:Cross-references: EMBL:X06143; NID:g54223; PIDN:CAA29500.1; PID:g54224
R:Seewell, W.A.; Brown, M.H.; Owen, M.J.; Fink, P.J.; Kozak, C.A.; Crumpton, M.J.
Eur. J. Immunol. 17, 1015-1020, 1987
A:Title: The murine homologue of the T lymphocyte CD2 antigen: molecular cloning, c
A:Reference number: S02293; MUID:87276135; PMID:2440689
A:Accession: S02293
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127, 'M', 129-174, 'N', 176-191, 'M', 193-344 <SEM>
A:Cross-references: EMBL:X00023; NID:g50346; PIDN:CAA68258.1; PID:g50347
C:Genetics:
A:Map position: 3
C:Superfamily: T-cell surface glycoprotein CD2
C:Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F:23-203/Domain: extracellular #status predicted <EXT>
F:204-228/Domain: transmembrane #status predicted <TM>
F:229-344/Domain: intracellular #status predicted <INT>

Query Match 12.4%; Score 80.5; DB 2; Length 344;
Best Local Similarity 27.4%; Pred. No. 0.95;
Matches 31; Conservative 15; Mismatches 46; Indels 21; Gaps 5;

OY 3 REDAFITGYGPKKGHSYTTAEAGIGITLVYIGVLLITGWCRRRNGRRLMDKSL 62
DB 188 KESTEVNCPKGLSF-YVTGVGAG-GLLVTL-VALFIPC-ICKRRRRRRRDEEL 243

OY 63 HVTQCALTRRCPOGPFDRDSKVSLOEKNCBPVVPNAPEYKLSAQSPP 115
DB 244 EI-----KASRTSVYERGPFPSTPAQAQNSVALQAPPP 279

RESULT 5
I49585
CD2 antigen protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49585
R:Yagita, H.; Okumura, K.; Nakauchi, H.
J. Immunol. 140, 1321-1326, 1988
A:Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule
A:Reference number: I49585; MUID:88140313; PMID:3257775
A:Accession: I49585
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <RES>
A:Cross-references: GB:M18934; NID:g192486; PIDN:AAA37397.1; PID:g309158
C:Superfamily: T-cell surface glycoprotein CD2

Query Match 12.4%; Score 80.5; DB 2; Length 344;
Best Local Similarity 27.4%; Pred. No. 0.95;
Matches 31; Conservative 15; Mismatches 46; Indels 21; Gaps 5;

OY 3 REDAFITGYGPKKGHSYTTAEAGIGITLVYIGVLLITGWCRRRNGRRLMDKSL 62
DB 188 KESTEVNCPKGLSF-YVTGVGAG-GLLVTL-VALFIPC-ICKRRRRRRRDEEL 243

OY 63 HVTQCALTRRCPOGPFDRDSKVSLOEKNCBPVVPNAPEYKLSAQSPP 115
DB 244 EI-----KASRTSVYERGPFPSTPAQAQNSVALQAPPP 279

RESULT 6

T49773

related to actin-interacting protein AIP3 [Imported] - Neurospora crassa

N:Alternate names: protein B9J10.100

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Farthmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49773

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-972 <SCH>

A:Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.100

A:Experimental source: BAC clone B9J10; strain OR74A

C:Genetics:

A:Gene: NCSP:B9J10.100

A:Map position: 6

A:introns: 29/3; 161/1; 329/1

Query Match

Best Local Similarity 12.2%; Score 79; DB 2; Length 972;
Matches 26; Conservative 10; Mismatches 31; Indels 18; Gaps 4;

QY 52 NGYR-ALMDKSLHVG-TQCALTRRCQEGFHDHDSKVSLOE-----KNC----- 93

DB 165 NGYRDSFRDSDSRNSGPTTASPTRRLPDSORDSGSVSDSSLSNTMNPVAPYPG 224

QY 94 EPVVPNAPYAEKLSAEPSPYSP 118

DB 225 ERTPTGPPAPPEINVDNFPPEPP 249

RESULT 7

E69665

nitrate reductase (EC 1.7.99.4) nsc - Bacillus subtilis

N:Alternate names: assimilatory nitrate reductase; nitrate reductase (narb)

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: E69665; 140028

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bettec

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallet

leach, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.M.; Portetelle

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zimstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram positive bacterium Bacillus subtilis.

A:Reference number: A69580; M01D:96044033; PMID:9384377

A:Accession: E69665

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-710 <KUN>

A:Cross-references: GB:299105; GB:AL009126; NID:g2632457; PIDN:CAB12125.1; PID:g2632617

A:Experimental source: Strain 168

R:Ogasawara, N.; Fujita, Y.; Kobayashi, Y.; Sadale, Y.; Tanaka, T.; Takahashi, H.; Yamat

Microbiology 141, 257-259, 1995

A:Title: Systematic sequencing of the Bacillus subtilis genome: progress report of the

A:Reference number: 139887; M01D:95219077; PMID:7704252

A:Accession: 140028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Gene: nsc

C:Superfamily: formate dehydrogenase

C:Keywords: 4Fe-4S; chromoprotein; iron-sulfur protein; metalloprotein; molybdenum

F;26/29/33/63/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

F;154/Binding site: molybdopterin (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 11.9%; Score 77; DB 2; Length 710;
Matches 34; Conservative 8; Mismatches 37; Indels 26; Gaps 6;

QY 15 KGHGSHYTAEE-----AAGIGILVILGVLILICWY--CRRNGYRALMDKSLHVG 66

DB 507 KGRYSYTAEDIFNELRBSRG-----GIDYSGISYGRRLREGIHPCEBSPG 560

QY 67 QCALTRRCQEGFHDHDSKVSLOEKNCPEVPNAPPA-YEKLSAE 110

DB 561 GLFT-----ESFAHDDQALAS-----VTFNEPVPEKPYAD 594

RESULT 8

T00043

BH-protocadherin-a - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999

C:Accession: T00043

R:Yoshida, K.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z14075

A:Accession: T00043

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1069 <YOS>

A:Cross-references: EMBL:AB006758; NID:d1227200; PIDN:BAA32597.1; PID:d1033562

C:Genetics:

A:Gene: pcdh7

A:Map position: 5C3-D

Query Match

Best Local Similarity 11.2%; Score 73; DB 2; Length 1069;
Matches 30; Conservative 15; Mismatches 32; Indels 40; Gaps 6;

QY 9 IYGRKKGHSYTTAEBAAGI-----GILVILGVLILICWYCR--RRNGYRALMDK 60

DB 865 IAGHG-----SYEISKRLSLIVIGVAGIMVILITLIVMARCYRSKKNKGYEA---- 914

QY 61 SLHVGTCALTRRCQEGFHDHDSKVSLOEKNCPEVPNAPPA-YEKLSAEQSPYSP 117

DB 915 -----GKK-----DHEDEFTPOQHDK-----SKRPKDKKRNKSKOPLYS 949

RESULT 9

T13720

gene expanded protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 17-Nov-2000

C:Accession: T13720

R:Boedighemier, M.; Laughton, A.

A:Title: Expanded: a gene involved in the control of cell proliferation in Imagina

A:Reference number: Z17740; M01D:94094747; PMID:8269855

A:Accession: T13720

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1429 <BOE>

A:Cross-references: EMBL:L14768; NID:g1763686; PID:g1763687; PIDN:AAB39774.1

C:Genetics:

A:Gene: expanded

A:Cross-references: FlyBase:FBgn0004583

C:Function:

A:Description: involved in control of cell proliferation in imaginal disk

Query Match

Best Local Similarity 11.2%; Score 72.5; DB 2; Length 1429;
Matches 23.4%; Pred. No. 30;

```

Matches 37; Conservative 10; Mismatches 52; Indels 59; Gaps 7;
QY 2 PREDAHFTYGPYKKGH-----HSTTAEEAGIGLTVLLIGTCYCRKRGY 54
DB 708 PRDSNVTSGSPRGDSDPTDNKHSLSAEELN-----LIVG-----KCTY 750
QY 55 --PALMDKSLH-----VGTQCALTRRCPOEGFDRHDSKVSU-----88
DB 751 PSKRTVSSLSHSCDDYTLPLGDDGEEFVDPPAPPPYSARHKETGLCGPIAKPIPKP 810
QY 89 -----QEKCEPVPVNPAP-PAYEKLSAEGSPPPYS 117
DB 811 IAAVAPKPDSPCSPVPVPAPIPAPPIARRRDPPEYS 848

RESULT 10
T51314
Probable CO-induced hydrogenase complex chain COOM [Imported] - Rhodospirillum rubrum
C:Species: Rhodospirillum rubrum
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51314
R:Kerby, R.L.
Submitted to the EMBL Data Library, July 1996
A:Reference number: 225372
A:Accession: T51314
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1265 <KER>
A:Cross-references: EMBL:U06510; PIDN:AA045116.1
A:Experimental source: strain URI
A:Gene: coom

Query Match 11.0%; Score 71.5; DB 2; Length 1265;
Best Local Similarity 30.9%; Pred. No. 33;
Matches 25; Conservative 8; Mismatches 33; Indels 15; Gaps 3;
QY 1 MPREDAHFTYGPYKKGHSTTAEEAGIGLTVLLIGTCYCRKRGYRDMK 60
DB 1172 LPVTEASWLGGLPEPGWHPLT-----LTALGAVGLIGWLC--RDGYRHRAAS 1219
QY 61 SLH---VGTQCALTRRCPOEG 78
DB 1220 TTHSCGVSDIAASAMHVPASG 1240

RESULT 11
T00041
BH-Protocadherin PCDH7 (clone BH-Pcdh-b) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 01-Dec-2000
C:Accession: T00041; T00040
R:Yoshida, K.; Yoshitomo-Nakagawa, K.; Seki, N.; Sasaki, M.; Sugano, S.
Genomics 49, 458-461, 1998
A:Title: Cloning, expression analysis, and chromosomal localization of BH-Protocadherin
A:Reference number: Z14074; MUID:98277460; PMID:9615233
A:Accession: T00041
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1072 <YOS>
A:Cross-references: EMBL:AB006756; NID:g2979419; PIDN:BA025195.1; PID:g2979420
A:Experimental source: clone BH-Pcdh-b
A:Accession: T00040
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1058, 'M', 1060, 'LH', 1063, 'Y', 1065, 'TVFG' <YOS>
A:Cross-references: EMBL:AB006755; NID:g2979417; PIDN:BA025194.1; PID:g2979418
A:Experimental source: clone BH-Pcdh-a
A:Map position: 4p15

Query Match 10.9%; Score 71; DB 2; Length 1072;
Best Local Similarity 25.5%; Pred. No. 31;

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Matches 27; Conservative 14; Mismatches 31; Indels 34; Gaps 5;
QY 20 STTAEBAAGI-----GILTVILGVLIGTCYCR--RRNGTRALMDKSLHVGTCALT 71
DB 870 SYEISKQRLSTIVGAVAGIMTVILITLIVMARCYSKRNKNGEYEA-----GKR-----917
QY 72 RRCPOEGFDRHDSKVSLOEKNEPVPVNPAPPAYEKLSAEGSPPPYS 117
DB 918 -----DHEDFTFPQOHDK-----SKPKKDKKRNKSKOPLYS 949

RESULT 12
T00042
BH-Protocadherin PCDH7 (clone BH-Pcdh-c) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00042
R:Yoshida, K.; Yoshitomo-Nakagawa, K.; Seki, N.; Sasaki, M.; Sugano, S.
Genomics 49, 458-461, 1998
A:Title: Cloning, expression analysis, and chromosomal localization of BH-Protocadherin
A:Reference number: Z14074; MUID:98277460; PMID:9615233
A:Accession: T00042
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1200 <YOS>
A:Cross-references: EMBL:AB006757; NID:g2979421; PIDN:BA025196.1; PID:g2979422
A:Experimental source: clone BH-Pcdh-c
A:Gene: c
A:Map position: 4p15

Query Match 10.9%; Score 71; DB 2; Length 1200;
Best Local Similarity 25.5%; Pred. No. 35;
Matches 27; Conservative 14; Mismatches 31; Indels 34; Gaps 5;

```

```

QY 20 STTAEBAAGI-----GILTVILGVLIGTCYCR--RRNGTRALMDKSLHVGTCALT 71
DB 823 SYEISKQRLSTIVGAVAGIMTVILITLIVMARCYSKRNKNGEYEA-----GKR-----870
QY 72 RRCPOEGFDRHDSKVSLOEKNEPVPVNPAPPAYEKLSAEGSPPPYS 117
DB 871 -----DHEDFTFPQOHDK-----SKPKKDKKRNKSKOPLYS 902

RESULT 13
H83334
Probable transcription regulator PA2488 [Imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83334
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.;
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <STO>
A:Cross-references: GB:AE004676; GB:AE004091; NID:g9948532; PIDN:AA05876.1; GSPDB:
A:Experimental source: strain PA01
A:Gene: PA2488

Query Match 10.9%; Score 70.5; DB 2; Length 254;
Best Local Similarity 25.7%; Pred. No. 7.9;
Matches 27; Conservative 11; Mismatches 40; Indels 27; Gaps 5;
QY 2 PREDAHFTYGPYKKGH-----SYTAEBAAGI-----GILTVILGVLIGTCYCR--RRNGTRALMDKSLHVGTCALT 71
DB 53 PROIMWIPGPHSHSHSLAGWSAYLAHECRDLPFRHGVYLACSAFVALIVERATRPW 112
QY 44 --GCWYCRRRNGYRALMDKSLHVGTCALTRRCPOEGFDRHDSKV 86

```

```

Db      113 TGSAMSTERENLLRVLLDELRLHAAVQ---RTRLRYPG---DSRL 150
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 14

688640
protein F52C12.3 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: 688640
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: A platform for investigating biology
A:Reference number: A75000; MID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: 688640.
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAC68961.1; PID:g3800953; GSPDB:GN00022; CESP:F52C12.3
C:Genetics:
A:Gene: F52C12.3
A:Map position: 4

RESULT 15

H84512
hypothetical protein At2g14000 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84512
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, R.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, D.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-766, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84512
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-346 <STO>
A:Cross-references: GB:AE002093; NID:g4388823; PIDN:ADD19778.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g14000
A:Map position: 2

Db 331 GASTSQPPPHS 342

Search completed: October 7, 2003, 18:49:41
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 18:39:49 : Search time 41 Seconds
(without alignments) 456.823 Million cell updates/sec

Title: US-09-898-860-2
Perfect score: 649
Sequence: 1 MPREDAHFTYGYRKKGHS.....NAPPAVEKLSAESPPPYSP 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	118	15	AAR63158 Tumour rejection a
2	649	100.0	118	16	AAR84212 MART-1 melanoma an
3	649	100.0	118	20	AAV42634 Human melanoma ant
4	649	100.0	118	20	AAW83134 Human tumour rejec
5	649	100.0	118	22	AAU28888 MART-1 antigen. H
6	649	100.0	118	22	AAW86042 Human MART1/Melana
7	649	100.0	118	23	AAU77793 Human melanoma ant
8	649	100.0	118	23	AAU84804 Human MART consens
9	649	100.0	118	23	AAU11541 Human Melanoma tum

10	649	100.0	119	20	AAV42633 Human melanoma ant
11	649	100.0	140	24	ABG76339 Recombinant mouse
12	649	100.0	496	24	ABG76343 Mouse recombinant
13	645	99.4	118	23	AAU77810 Human MART-1 prote
14	645	99.1	118	23	AAU77809 Human MART-1 prote
15	642	98.9	118	20	AAV31980 Human MART1 melano
16	641	98.8	118	23	AAU77806 Human MART-1 prote
17	641	98.8	118	23	AAU77808 Human MART-1 prote
18	641	98.8	118	23	AAU77811 Human MART-1 prote
19	640	98.6	118	23	AAU77807 Human MART-1 prote
20	599	92.3	118	23	AAU77815 Human MART-1 prote
21	598	92.1	118	23	AAU77813 Human MART-1 prote
22	598	92.1	118	23	AAU77814 Human MART-1 prote
23	597	92.0	118	23	AAU77812 Human MART-1 prote
24	596	91.8	118	23	AAU77816 Human MART-1 prote
25	562	86.6	104	23	AAU98926 Human melanoma ant
26	532	82.0	98	23	ABG70354 Novel human thromb
27	427.5	65.9	113	20	AAV31979 Mouse MART1 melano
28	427.5	65.9	114	20	AAV42632 Murine melanoma an
29	323	40.8	94	23	ABG70355 Novel human Thromb
30	262.5	40.4	5546	23	AAU85008 Human MART segment
31	209	32.2	40	22	AAU85008 Human MART segment
32	173	26.7	30	23	AAU84868 Human MART segment
33	169	26.0	30	23	AAU84870 Human MART segment
34	167	25.7	30	23	AAU84871 Human MART segment
35	163	25.1	30	23	AAU84869 Human MART segment
36	161	24.8	30	23	AAU84867 Human MART segment
37	158	24.3	30	23	AAU84865 Human MART segment
38	156	24.0	30	22	AAU84864 Human MART segment
39	148	22.8	30	23	AAU84866 Human MART segment
40	121	18.6	23	23	ABG79128 Human MART-1 class
41	108	16.6	21	18	AAU00903 Human melanoma MAR
42	108	16.6	21	18	AAE20402 Human melanoma tum
43	98	15.1	22	23	AAU11546 Human control pept
44	82	12.6	17	23	AAU84872 Human MART segment
45	79	12.2	1114	22	ABW66628 Drosophila melanog

ALIGNMENTS

RESULT 1	AAU63158	standard; Protein: 118 AA.
ID	AAU63158	
AC	AAU63158	
XX		
DT	25-MAR-2003 (updated)	
DT	26-MAY-1995 (first entry)	
XX		
DE	Tumour rejection antigen precursor.	
XX		
KW	Tumour rejection antigen; precursor; HLA-A2 molecule; tyrosinase;	
KW	isolation; melanoma; cell line; LB-39-MEL; diagnosis; vaccine;	
KW	therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9421126-A1.	
XX		
PD	29-SEP-1994.	
XX		
PF	09-MAR-1994; 94WO-US02487.	
XX		
PR	18-MAR-1993; 93US-0032978.	
XX		
PA	(LUDWIG-) LUDWIG INST CANCER RES.	
XX		
PI	Boon-Fallieur T, Brichard V, De Plaen E, Traversari C;	
PI	Van Pel A, Wolfel T;	
XX		
DR	WPI: 1994-316544/39.	
DR	N-PSDB; AAQ76370.	

XX Nucleic acid coding for a tumour rejection antigen precursor - is
 PT used for developing prods. for diagnosis or treatment of expression
 PT related disorders, partic. melanoma
 PS Claim 5; Page 14; 26pp; English.

CC This sequence represents the tumour rejection antigen precursor which is
 CC processed to a tumour rejection antigen presented by HLA-A2 molecules.
 CC The tumour rejection antigen is not related to tyrosinase. The CDNA
 CC encoding this sequence was isolated from the melanoma cell line,
 CC LB-39-MEL. The tumour rejection antigen may be used for diagnosis or
 CC in vaccines or for therapy of disorders characterised by the expression
 CC of the tumour rejection antigen precursor, particularly melanoma.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX

SQ Sequence 118 AA;

Query Match 100.0%; Score 649; DB 15; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.1e-65;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRDAHFHYGYPKKGHSYTTAEAGIGILTVILGVLLIGCWCRRRNGYRALMDK 60
 DB 1 MPRDAHFHYGYPKKGHSYTTAEAGIGILTVILGVLLIGCWCRRRNGYRALMDK 60

QY 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAQSPPPYSP 118
 DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAQSPPPYSP 118

RESULT 2

AAR84212
 ID AAR84212 standard; Protein; 118 AA.

AC AAR84212;

DE 20-APR-1996 (first entry)

XX MART-1 melanoma antigen.

XX MART-1; melanoma antigen recognised by T-cell; melanoma;

KW metastatic melanoma; tumour-associated antigen; immunogen;

KW diagnosis; prognosis; prophylaxis; therapy; vaccine.

OS Mammalian.

XX Key Location/Qualifiers
 XX Region 27..47
 XX /note="hydrophobic region"

PN W09529193-A2.

PD 02-NOV-1995.

PF 21-APR-1995; 95WO-US05063.

PR 05-APR-1995; 95US-0417174.

PR 22-APR-1994; 94US-0231365.

PA (USSH) US SEC DEPT HEALTH.

PI Kawakami Y, Rosenberg SA;

DR WPI; 1995-382963/49.

DR N-PSDB; AAT02714.

XX DNA encoding melanoma antigens recognised by T-lymphocytes - also
 PT vectors, host cells and antibodies, used to detect, treat and
 PT immunise animal against melanoma.

PS Claim 11; Page 117; 184pp; English.

CC The melanoma antigen (MART-1) is produced by recombinant DNA
 CC methods, i.e. preferably using a baculovirus vector for expression
 CC in insect cell cultures. MART-1 protein is a source of immunogenic
 CC peptides (see AAR84196 for peptide M9-2) which are optionally modified
 CC (see AAR84783-R84800) and used in medicaments for the treatment or
 CC prevention (by immunization) of melanoma. Antibodies against MART-1
 CC and its immunogenic peptides may be used in the detection and
 CC isolation of MART-1 from a sample, the detection of which is
 CC indicative of a disease state (melanoma or metastatic melanoma).
 CC
 XX

SQ Sequence 118 AA;

Query Match 100.0%; Score 649; DB 16; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.1e-65;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRDAHFHYGYPKKGHSYTTAEAGIGILTVILGVLLIGCWCRRRNGYRALMDK 60
 DB 1 MPRDAHFHYGYPKKGHSYTTAEAGIGILTVILGVLLIGCWCRRRNGYRALMDK 60

QY 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAQSPPPYSP 118
 DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAQSPPPYSP 118

RESULT 3

AA42634
 ID AA42634 standard; Protein; 118 AA.

AC AA42634;

DE 10-JAN-2000 (first entry)

XX Human melanoma antigen hMART1.

XX Immune response; self-antigen; immune effector cell; cancer; melanoma;

KW mouse; melanoma antigen; MART1.

XX Homo sapiens.

PN W09946988-A1.

PD 23-SEP-1999.

PF 19-MAR-1999; 99WO-US06034.

PR 20-MAR-1998; 98US-0078890.

PA (GENZ) GENZYME CORP.

PI Nicolette CA;

DR WPI; 1999-580277/49.

DR N-PSDB; AA207987.

XX Method of inducing an immune reaction to a self-antigen by
 PT administering the antigen, especially useful for treating cancer or
 PT melanoma

XX Disclosure; Fig 3A-B; 70pp; English.

CC The invention provides a method of inducing a prophylactic immune
 CC response to a self-antigen in a subject. The method comprises
 CC administering the antigen or its derivative or administering educated
 CC immune effector cells able to recognize and lyse cells expressing the
 CC self-antigen or its derivative. The method is used to stimulate an immune
 CC response against a self-antigen especially one expressed in a cancer or
 CC melanoma. The present sequence represents the human melanoma antigen
 CC hMART1.

SQ Sequence 118 AA;

Query Match 100.0%; Score 649; DB 20; Length 118;

ID AAB86042 standard; Protein: 118 AA.
XX
AC AAB86042;
XX
DT 16-JUL-2001 (first entry)
XX
DE Human MART1/Melana protein.
XX
KW Listeria: expression vector; tumor-associated antigen; Trp 1; Trp 2;
KW Melana/MART-1; cytosolic; attenuated; immunotherapy; malignant melanoma;
KW pigmented tumor; malignant schwannoma; vaccination; tyrosinase;
KW antigen-presenting cell.
XX
OS Homo sapiens.
XX
PN W0200127295-A1.
XX
PD 19-APR-2001.
XX
PE 13-OCT-2000; 2000WO-DE03629.
XX
PR 14-OCT-1999; 99DE-1049594.
XX
PI (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schenckendorf D, Paschen A, Chakraborty T, Dommann E;
XX
DR WPI: 2001-282041/29.
XX
DR N-PSDB; AAF86044.
XX
PT Listeria expression vector for immunotherapy, particularly of malignant
PT melanoma, comprises a DNA sequence encoding tumor-associated antigens -
XX
XX
PS Disclosure; Fig 4; 41pp: German.
XX
CC This invention describes a novel Listeria expression vector (A) for
CC immunotherapy which comprises a promoter (P), functional in Listeria,
CC operably linked to a DNA sequence (I) encoding one of the
CC tumor-associated antigens (II) human tyrosinase, Trp 1 or 2, or
CC Melana/MART-1. The products of the invention have cytostatic activity.
CC Recombinant attenuated Listeria containing (A) are useful for
CC immunotherapy (propylactic, adjuvant or therapeutic), specifically of
CC malignant melanoma (but also other pigmented tumors such as malignant
CC schwannoma), particularly as a replacement for radiotherapy. Using
CC attenuated Listeria as carrier for (A) provides a simple way of
CC vaccination, since antigen-presenting cells acquire tumor-associated
CC antigens by natural infection, eliminating the need for labor-intensive
CC ex vivo modification of autologous cells. This sequence represents the
CC human MART-1/Melana protein described in the method of the invention.
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 649; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.1e-65;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPREDAHFTYGYPKKGHSYTTAEAGIGITVTLIGVLLIGWCYCRRRNGYRALMDK 60
DB 1 MPREDAHFTYGYPKKGHSYTTAEAGIGITVTLIGVLLIGWCYCRRRNGYRALMDK 60
QY 61 SLHVGTCALTRRCPOEGFDRHDSKVSLOEKNCCEPVVNPAPAYEKLSAEOSSPPYSP 118
DB 61 SLHVGTCALTRRCPOEGFDRHDSKVSLOEKNCCEPVVNPAPAYEKLSAEOSSPPYSP 118
RESULT 7
AAU77793 ID AAU77793 standard; Protein: 118 AA.
XX
AC AAU77793;
XX
DT 05-JUN-2002 (first entry)
XX

DE Human melanoma antigen recognised by T cells (MART-1).
XX
KW MART-1; melanoma antigen recognised by T cells; human;
KW anti-melanoma peptide; major histocompatibility complex; MHC;
KW immunotherapy; cancer; vaccine; immunoregulatory.
XX
OS Homo sapiens.
XX
PN W0200212272-A2.
XX
PD 14-FEB-2002.
XX
PE 03-AUG-2001; 2001WO-US24328.
XX
PR 04-AUG-2000; 2000US-223641P.
XX
PR 13-DEC-2000; 2000US-255502P.
XX
PR 25-JAN-2001; 2001US-264432P.
XX
PR 26-MAR-2001; 2001US-279005P.
XX
PA (GENZ) GENZYME CORP.
XX
PI Nicolette CA;
XX
DR WPI: 2002-257459/30.
XX
DR N-PSDB; ABR11763.
XX
PT Novel anti-melanoma peptide compounds useful for inducing immune
PT response in a subject, and in the preparation of medicaments for the
PT treatment and diagnosis of cancer -
XX
XX
PS Disclosure; Page 69-70; 79pp: English.
XX
CC This invention relates to a novel anti-melanoma peptide compound
CC comprising a peptide of the human melanoma antigen recognised by T cells
CC (MART-1) protein. These compounds are designed to enhance binding to
CC major histocompatibility (MHC) compounds and enhance immunoregulatory
CC properties and induce an immune response. The invention also comprises
CC the nucleotide sequences encoding the peptides of the invention. The
CC compounds of the invention are useful for inducing an immune response in
CC a subject, by delivering the compounds in the context of a major
CC histocompatibility (MHC) molecule which presents the compound on the
CC surface of an antigen presenting cell, or by delivering it as a
CC polynucleotide that encodes the peptide. The invention also comprises
CC antibodies that recognise and bind these compounds which are useful in
CC immunotherapy. The compounds of the invention are useful for modulating
CC an immune response to synthetic and naturally occurring compounds in a
CC subject. The compounds may also be used as components of anti-cancer
CC vaccines and to expand immune effector cells that are specific for
CC cancers characterised by expression of the human melanoma antigen
CC recognised by T cells, MART-1. The compounds of the invention are also
CC useful for the detection and purification of antibodies and may be used
CC for the preparation of medicaments for the diagnosis and treatment of
CC diseases such as cancer. The compounds of the invention have enhanced
CC binding to MHC molecules and enhanced immunoregulatory properties
CC relative to their natural counterparts. The present sequence represents
CC the human melanoma antigen recognised by T cells (MART-1) used to create
CC the peptide compounds of the invention.
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 649; DB 23; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.1e-65;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPREDAHFTYGYPKKGHSYTTAEAGIGITVTLIGVLLIGWCYCRRRNGYRALMDK 60
DB 1 MPREDAHFTYGYPKKGHSYTTAEAGIGITVTLIGVLLIGWCYCRRRNGYRALMDK 60
QY 61 SLHVGTCALTRRCPOEGFDRHDSKVSLOEKNCCEPVVNPAPAYEKLSAEOSSPPYSP 118
DB 61 SLHVGTCALTRRCPOEGFDRHDSKVSLOEKNCCEPVVNPAPAYEKLSAEOSSPPYSP 118

RESULT 8
 ID AAU84804 standard; protein; 118 AA.
 XX AAU84804;
 AC
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human MART consensus sequence.
 XX
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.
 XX
 OS Homo sapiens.
 XX
 PN WO200190197-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 25-MAY-2001; 2001WO-AU00622.
 XX
 PR 26-MAY-2000; 2000AU-0007761.
 XX
 PA (AUS) UNIV AUSTRALIAN NAT.
 XX
 PI Thomson SA, Ramsay IA;
 XX
 DR WPI: 2002-147575/19.
 XX
 PT New synthetic polypeptides having several different segments of at
 PT least one parent polypeptide linked together differently compared to
 PT the linkage in the parent polypeptide, for inducing immune response
 PT against a pathogen or cancer
 XX
 PS Example 3; Fig 27; 364pp; English.
 XX
 CC The invention relates to a new synthetic polypeptide (1) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for
 CC designing the synthetic polypeptides. The synthetic polypeptides and
 CC polynucleotides are referred to as a Savine. The synthetic polypeptide is
 CC useful for modulating immune responses preferably directed against a
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present
 CC sequence is a consensus sequence for a parent protein used to design a
 CC savine of the invention.
 XX
 SQ Sequence 118 AA:
 Query Match 100.0%; Score 649; DB 23; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,1e-65;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPREDAHFYGYPKKGHSYTTAEAGIGLTVILGCVTCRCRRNGRAMDK 60
 DB 1 MPREDAHFYGYPKKGHSYTTAEAGIGLTVILGCVTCRCRRNGRAMDK 60
 QY 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOENKCEPVVPNAPYAEKLSAQSPPTSP 118

DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOENKCEPVVPNAPYAEKLSAQSPPTSP 118
 RESULT 9
 ID AAU1541 standard; protein; 118 AA.
 XX AAU1541;
 AC
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human Melanoma tumour associated antigen.
 XX
 KW Human; melanoma tumour associated antigen; human leukocyte antigen;
 KW major histocompatibility complex; MHC; HLA-A2.2; vaccine; cancer;
 KW HIV; human immunodeficiency virus infection; cytostatic; vitreolide;
 KW housekeeping epitope; adoptive immunotherapy; neoplastic disease;
 KW viral disease; hepatitis virus; papilloma virus; tumour; leukaemia;
 KW lymphoma; breast cancer; prostate cancer; lung cancer; melan A;
 KW parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.
 XX
 OS Homo sapiens.
 XX
 PN WO200182963-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13806.
 XX
 PR 28-APR-2000; 2000US-0560465.
 XX
 PR 28-APR-2000; 2000US-0561074.
 PR 28-APR-2000; 2000US-0561571.
 PR 28-APR-2000; 2000US-0561572.
 XX
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Sismard JDL, Diamond DC, Lei X;
 XX
 DR WPI: 2002-066492/09.
 XX
 PT Novel vaccine useful for treating neoplastic and viral diseases,
 PT comprises a first housekeeping epitope derived from a first antigen
 PT associated with a first target cell
 XX
 PS Example 21; Fig 15; 131pp; English.
 XX
 CC The invention relates to a vaccine comprising a first housekeeping
 CC epitope derived from a first antigen associated with a first target
 CC cell. Also included are an isolated T cell expressing a T cell receptor
 CC specific for a major histocompatibility complex (MHC)-peptide complex
 CC comprising a first housekeeping epitope which is derived from a first
 CC antigen associated with a first target cell, selecting an epitope
 CC (or peptide sequence) from a population of peptide fragments of an
 CC antigen associated with a target in a host, where the fragments have a
 CC known or predicted affinity for a MHC receptor peptide binding cleft of
 CC the host, where the epitope selected corresponds to a product of
 CC a nucleolytic cleavage of the antigen in a cell of the host and
 CC a nucleic acid construct comprising a first coding region, where the
 CC first coding region comprises a first sequence encoding at least a first
 CC polypeptide, where the first polypeptide comprises a first housekeeping
 CC epitope derived from a first antigen associated with a first target cell;
 CC The epitopes, peptides, vaccines and nucleic acids are useful in the
 CC manufacture of a medicament for use in adoptive immunotherapy and for
 CC prevention and treatment of neoplastic and viral diseases (e.g.
 CC human immunodeficiency virus, HIV, infection, hepatitis virus and
 CC papilloma virus), cancers (e.g. tumours, leukaemia, lymphoma, breast
 CC cancer, prostate cancer and lung cancer), infection of cells by
 CC intracellular parasites (e.g. Chlamydia, Trypanosoma and
 CC Toxoplasma) and many other examples given in the specification.
 CC The invention permits the vaccine designer to ignore peptides that,
 CC despite predicted high binding affinity for MHC, will never be useful
 CC because they cannot be presented by target cells. The invention provides

CC a major advance in vaccine design, one that combines the power of antigen
CC sequence analysis with the fundamental realities of immunology. The
CC invention allows for the simple and effective selection of meaningful
CC epitopes for creation of MHC class I or Class II vaccines using any
CC polypeptide sequence corresponding to a desired target. The present
CC sequence is an HLA-A2.1 (human leukocyte antigen) presenting target cell.
CC protein from which epitopes of the invention may be derived, Mela-A
CC (melanoma tumour associated antigen).

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 649; DB 23; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.1e-65;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60
DB 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60

OY 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAEQSPPPYSP 118
DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAEQSPPPYSP 118

RESULT 10

AA42633
ID AAY42633 standard; Protein: 119 AA.

XX AC AAY42633;

XX DT 10-JAN-2000 (first entry)

XX DE Human melanoma antigen hMART1.

XX KW Immune response; self-antigen; immune effector cell; cancer; melanoma;
XX mouse; melanoma antigen; MART1.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT MISC-difference 119 /note= "unspecified"

XX PN MO9946988-A1.

XX PD 23-SEP-1999.

XX PF 19-MAR-1999; 99WCO-US06034.

XX PR 20-MAR-1998; 98US-0078890.

XX PA (GENZ) GENZYME CORP.

XX PI Nicotlette CA;

XX DR WPI: 1999-580277/49.

XX DR N-PSDB; AAZ07986.

XX PT Method of inducing an immune reaction to a self-antigen by
XX administering the antigen, especially useful for treating cancer or
XX melanoma

XX PS Disclosure; Fig 2B; 70pp; English.

XX CC The invention provides a method of inducing a prophylactic immune

XX CC response to a self-antigen in a subject. The method comprises

XX CC administering the antigen or its derivative or administering educated

XX CC immune effector cells able to recognize and lyse cells expressing the
XX CC self-antigen or its derivative. The method is used to stimulate an immune
XX CC response against a self-antigen especially one expressed in a cancer or
XX CC melanoma. The present sequence represents the human melanoma antigen
XX CC hMART1.

SQ Sequence 119 AA;

Query Match 100.0%; Score 649; DB 20; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e-65;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60
DB 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60

OY 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAEQSPPPYSP 118
DB 61 SLHVGTCALTRRCPOEGFDHRDSKVSLOEKNCPEVVPNAPPAYEKLSAEQSPPPYSP 118

RESULT 11

ABG76339
ID ABG76339 standard; Protein: 140 AA.

XX AC ABG76339;

XX DT 10-MAY-2003 (first entry)

XX DE Recombinant mouse protein, Melana/MART1.

XX KW Mouse; protein targeting; exosome; lactadherin; C1 domain; C2 domain;
XX membrane vesicle; mutant; mutlein.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO2003016522-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-EP09108.

XX PR 17-AUG-2001; 2001US-313159P.

XX PR 26-DEC-2001; 2001US-343991P.

XX PA (ANOS) ANOSYS INC.

XX PI Delcayre A, Le Pecq J;

XX DR WPI: 2003-268331/26.

XX PT Targeting polypeptides to exosomes providing a chimeric genetic
XX construct and introducing the construct into exosome-producing cells in
XX vivo or ex vivo

XX PS Example 6; Page 85-86; 94pp; English.

XX CC The present invention relates to a method and compounds for targeting

XX CC polypeptides to exosomes. The method comprises providing a chimeric

XX CC genetic construct encoding the polypeptide fused to a targeting

XX CC polypeptide comprising lactadherin or its portion comprising

XX CC a functional C1 and/or C2 domain, and introducing the construct into

XX CC exosome-producing cells in vivo or ex vivo, to generate recombinant

XX CC vesicles. The method is useful for targeting proteins to membrane

XX CC vesicles, particularly exosomes, and is useful in experimental,
XX CC research, therapeutic, prophylactic, and diagnostic areas. The
XX CC present sequence represents a recombinant mouse protein.

SQ Sequence 140 AA;

Query Match 100.0%; Score 649; DB 24; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60
DB 1 MPREDAHFIYGYPKKGHSHTTAEBAAGIGILTVILGVLLIGCWYCRRRNGRYALMDK 60

QY 61 SLHVGTCALTRRCPOGEGFDRHDSKVSIOEKNCPEVVPNAPPAYEKLSAEO\$PPPYSP 118
 DB 61 SLHVGTCALTRRCPOGEGFDRHDSKVSIOEKNCPEVVPNAPPAYEKLSAEO\$PPPYSP 118

RESULT 12

ABG76343 standard; Protein; 496 AA.

AC ABG76343;

DT 10-MAY-2003 (first entry)

DE Mouse recombinant chimeric fusion protein, MAR1/CCR7.

KW Mouse; protein targeting; exosome; lactadherin; C1 domain; C2 domain;
 membrane vesicle; mutant; mutein.

OS Mus sp.

PN WO2003016522-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-EP09108.

PR 17-AUG-2001; 2001US-313159P.

PR 26-DEC-2001; 2001US-343991P.

PA (ANOS-) ANOSYS INC.

PI Delcayre A, Le Pecq J;

DR WPI; 2003-268331/26.

PT Targeting polypeptides to exosomes providing a chimeric genetic
 construct and introducing the construct into exosome-producing cells in
 vivo or ex vivo

PS Claim 28; Page 90-92; 94pp; English.

CC The present invention relates to a method and compounds for targeting
 CC polypeptides to exosomes. The method comprises providing a chimeric
 CC genetic construct encoding the polypeptide fused to a targeting
 CC polypeptide comprising lactadherin or its portion comprising
 CC a functional C1 and/or C2 domain, and introducing the construct into
 CC exosome-producing cells in vivo or ex vivo, to generate recombinant
 CC exosomes. The method is useful for targeting proteins to membrane
 CC vesicles, particularly exosomes, and is useful in experimental,
 CC research, therapeutic, prophylactic, and diagnostic areas. The
 CC present sequence represents a mouse recombinant chimeric fusion
 CC protein.

SQ Sequence 496 AA;

Query Match 100.0%; Score 649; DB 24; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.3e-64;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPREDFAFIYGYPRKGGHSTYTAEEAAGIGILVYILGCVLCGRNRNGYRALMDK 60
 DB 1 MPREDFAFIYGYPRKGGHSTYTAEEAAGIGILVYILGCVLCGRNRNGYRALMDK 60
 QY 61 SLHVGTCALTRRCPOGEGFDRHDSKVSIOEKNCPEVVPNAPPAYEKLSAEO\$PPPYSP 118
 DB 61 SLHVGTCALTRRCPOGEGFDRHDSKVSIOEKNCPEVVPNAPPAYEKLSAEO\$PPPYSP 118

RESULT 13
 AAU77810
 ID AAU77810 standard; Protein; 118 AA.

AC AAU77810;
 DT 05-JUN-2002 (first entry)
 DE Human MAR1-1 protein mutant #5.
 KW MAR1-1; melanoma antigen recognised by T cells; human; mutant;
 immunotherapy; cancer; vaccine; immunoregulatory; mutein.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Misc-difference 27 /note= "Wild type A substituted by T"
 FT Misc-difference 28 /note= "Wild type A substituted by A"
 PN WO200212272-A2.
 PD 14-FEB-2002.
 PF 03-AUG-2001; 2001WO-US24328.
 PR 04-AUG-2000; 2000US-223641P.
 PR 13-DEC-2000; 2000US-255502P.
 PR 25-JAN-2001; 2001US-264432P.
 PR 26-MAR-2001; 2001US-279005P.
 PA (GENZ) GENZYME CORP.
 PI Nicolette CA;
 DR WPI; 2002-257459/30.
 PT Novel anti-melanoma peptide compounds useful for inducing immune
 PT response in a subject, and in the preparation of medicaments for the
 PT treatment and diagnosis of cancer
 PS Claim 16; Page -: 79pp; English.
 CC This invention relates to a novel anti-melanoma peptide compound
 CC comprising a peptide of the human melanoma antigen recognised by T cells
 CC (MAR1-1) protein. These compounds are designed to enhance binding to
 CC major histocompatibility (MHC) compounds and enhance immunoregulatory
 CC properties and induce an immune response. The invention also comprises
 CC the nucleotide sequences encoding the peptides of the invention. The
 CC compounds of the invention are useful for inducing an immune response in
 CC a subject, by delivering the compounds in the context of a major
 CC histocompatibility (MHC) molecule which presents the compound on the
 CC surface of an antigen presenting cell, or by delivering it as a
 CC polynucleotide that encodes the peptide. The invention also comprises
 CC antibodies that recognise and bind these compounds which are useful in
 CC immunotherapy. The compounds of the invention are useful for modulating
 CC an immune response to synthetic and naturally occurring compounds in a
 CC subject. The compounds may also be used as components of anti-cancer
 CC vaccines and to expand immune effector cells that are specific for
 CC cancers characterised by expression of the human melanoma antigen
 CC recognised by T cells, MAR1-1. The compounds of the invention are also
 CC useful for the detection and purification of antibodies and may be used
 CC for the preparation of medicaments for the diagnosis and treatment of
 CC diseases such as cancer. The compounds of the invention have enhanced
 CC binding to MHC molecules and enhanced immunoregulatory properties
 CC relative to their natural counterparts. The present sequence represents
 CC the human melanoma antigen recognised by T cells (MAR1-1) mutant #5 of
 CC the invention. This mutant has amino acid alterations in the region
 CC corresponding to the MHC class I binding site, these mutations confer
 CC tighter binding to the MHC.
 CC Note: This sequence is not shown in the specification but was created by
 CC the indexer from the wild type sequence shown in AAU7793 and the
 CC information given in claim 16 of the specification.
 SQ Sequence 118 AA;

Query Match 99.4%; Score 645; DB 23; Length 118;
 Best Local Similarity 99.2%; Pred. No. 66-65;
 Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MPRDAHFITYGPKKGHSYTTAEBAAGIGITVLIGVLLIGCWCRRRNGRYALMDK 60
 |||||
 DB 1 MPRDAHFITYGPKKGHSYTTAEBAAGIGITVLIGVLLIGCWCRRRNGRYALMDK 60
 |||||

OY 61 SLHVGTCALTRRCPOEGFDHRDSKYSLOEKNCPEVVPNAPPAVEKLSAQSPPPYSP 118
 |||||
 DB 61 SLHVGTCALTRRCPOEGFDHRDSKYSLOEKNCPEVVPNAPPAVEKLSAQSPPPYSP 118
 |||||

RESULT 14
 AAU77809-
 ID AAU77809 standard; Protein; 118 AA.
 XX AAU77809;
 AC
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human MART-1 protein mutant #4.
 XX
 XX MART-1; melanoma antigen recognised by T cells; human; mutant;
 KW anti-melanoma peptide; major histocompatibility complex; MHC;
 KW immunotherapy; cancer; vaccine; immunoregulatory; mutcin.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27
 FT /note= "Wild type A substituted by F"
 FT Misc-difference 28
 FT /note= "Wild type A substituted by A"
 XX
 FT
 XX WO200212272-A2.
 XX
 XX
 XX 14-FEB-2002.
 XX
 XX
 XX 03-AUG-2001; 2001WO-US24328.
 XX
 XX
 XX 04-AUG-2000; 2000US-223641P.
 PR 13-DEC-2000; 2000US-255502P.
 PR 25-JAN-2001; 2001US-264432P.
 PR 26-MAR-2001; 2001US-279005P.
 XX
 XX (GENZ) GENZYME CORP.
 XX
 XX
 XX Nicolette CA;
 XX
 XX
 XX WPI: 2002-257459/30.
 XX
 XX
 XX Novel anti-melanoma peptide compounds useful for inducing immune
 FT response in a subject, and in the preparation of medicaments for the
 PT treatment and diagnosis of cancer
 XX
 XX
 PS Claim 15; Page -: 79pp; English.
 XX
 XX This invention relates to a novel anti-melanoma peptide compound
 CC comprising a peptide of the human melanoma antigen recognised by T cells
 CC (MART-1) protein. These compounds are designed to enhance binding to
 CC major histocompatibility (MHC) compounds and enhance immunoregulatory
 CC properties and induce an immune response. The invention also comprises
 CC the nucleotide sequences encoding the peptides of the invention. The
 CC compounds of the invention are useful for inducing an immune response in
 CC a subject, by delivering the compounds in the context of a major
 CC histocompatibility (MHC) molecule which presents the compound on the
 CC surface of an antigen presenting cell, or by delivering it as a
 CC polynucleotide that encodes the peptide. The invention also comprises
 CC antibodies that recognise and bind these compounds which are useful in
 CC immunotherapy. The compounds of the invention are useful for modulating
 CC an immune response to synthetic and naturally occurring compounds in a

CC subject. The compounds may also be used as components of anti-cancer
 CC vaccines and to expand immune effector cells that are specific for
 CC cancers characterised by expression of the human melanoma antigen
 CC recognised by T cells. MART-1. The compounds of the invention are also
 CC useful for the detection and purification of antibodies and may be used
 CC for the preparation of medicaments for the diagnosis and treatment of
 CC diseases such as cancer. The compounds of the invention have enhanced
 CC binding to MHC molecules and enhanced immunoregulatory properties
 CC relative to their natural counterparts. The present sequence represents
 CC the human melanoma antigen recognised by T cells (MART-1) mutant #4 of
 CC the invention. This mutant has amino acid alterations in the region
 CC corresponding to the MHC class I binding site, these mutations confer
 CC tighter binding to the MHC.
 CC Note: This sequence is not shown in the specification but was created by
 CC the indexer from the wild type sequence shown in AAU77793 and the
 CC information given in claim 15 of the specification.
 XX
 XX
 XX Sequence 118 AA;
 SQ

Query Match 99.1%; Score 643; DB 23; Length 118;
 Best Local Similarity 99.2%; Pred. No. 1e-64;
 Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MPRDAHFITYGPKKGHSYTTAEBAAGIGITVLIGVLLIGCWCRRRNGRYALMDK 60
 |||||
 DB 1 MPRDAHFITYGPKKGHSYTTAEBAAGIGITVLIGVLLIGCWCRRRNGRYALMDK 60
 |||||

OY 61 SLHVGTCALTRRCPOEGFDHRDSKYSLOEKNCPEVVPNAPPAVEKLSAQSPPPYSP 118
 |||||
 DB 61 SLHVGTCALTRRCPOEGFDHRDSKYSLOEKNCPEVVPNAPPAVEKLSAQSPPPYSP 118
 |||||

RESULT 15
 AAU31980
 ID AAU31980 standard; Protein; 118 AA.
 XX AAU31980;
 AC
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Human MART1 melanocyte differentiation antigen.
 XX
 XX MART1; melanocyte differentiation antigen; melanoma; human;
 KW antigen presentation; adoptive immunotherapy; cancer; therapy;
 KW vaccine.
 XX
 XX Homo sapiens.
 OS
 XX
 XX
 XX W09947102-A2.
 XX
 XX
 XX 23-SEP-1999.
 XX
 XX
 XX 19-MAR-1999; 99WO-US06031.
 PF
 XX
 XX 20-MAR-1998; 98US-0078880.
 PR
 XX
 XX (GENZ) GENZYME CORP.
 XX
 XX
 XX Nicolette CA, Kaplan J;
 XX
 XX
 XX WPI: 1999-590956/50.
 DR N-PSDS; AAU20065.
 XX
 XX
 XX Preparing cells for use as cancer vaccines and in adoptive
 PT immunotherapy
 XX
 XX
 PS Disclosure; Page 51; 55pp; English.
 XX
 XX The present sequence represents human MART1, a melanocyte
 CC differentiation antigen that is specifically recognised by HLA-A2
 CC restricted tumour-infiltrating lymphocytes of melanoma patients.
 CC The invention provides methods for immunotherapy, in particular for
 CC inducing an immune response against an antigen in a patient.

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OM protein - protein search, using sw model

Run on: October 7, 2003, 18:43:14 : Search time 33 Seconds

(without alignments) 922.734 Million cell updates/sec

Title: US-09-898-860-2

Perfect score: 649

Sequence: 1 MPREDAHFITYGPKKGHS.....NAPPAYEKLSAEQSPPPYSP 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420.5	64.8	113	11	Q9DIY3
2	87	13.4	4957	4	014687
3	87	13.4	5262	4	014686
4	81	12.5	2034	2	093NX7
5	80.5	12.4	344	11	Q9R201
6	80.5	12.4	1127	3	Q9P571
7	79.5	12.2	494	15	0994J1
8	78	12.0	540	17	08TUC3
9	78	12.0	1814	10	08M5N5
10	77	11.9	488	4	08N504
11	77	11.9	491	4	08RBU7
12	77	11.9	750	10	09AUC2
13	76	11.7	303	4	09UKJ1
14	75.5	11.6	227	4	09UKJ0
15	75	11.6	107	12	09J455
16	75	11.6	107	12	086198

17	74.5	11.5	496	15	08UT44	08UT44 human immu
18	74	11.4	739	5	08IGR9	08IGR9 drosophila
19	74	11.4	883	5	09YBN1	09YBN1 drosophila
20	73.5	11.3	198	11	Q8R182	Q8R182 mus musculu
21	73	11.2	301	5	Q8MY26	Q8MY26 papilio xut
22	73	11.2	1069	11	088185	088185 mus musculu
23	72.5	11.2	393	6	08MK55	08MK55 cyclopes dl
24	72.5	11.2	405	3	08J221	08J221 glarex lozo
25	72.5	11.2	1427	5	Q9VPO0	Q9VPO0 drosophila
26	72	11.1	1729	10	Q8R2W5	Q8R2W5 oryza sativ
27	71.5	11.0	1265	2	P72316	P72316 rhodospiril
28	71	10.9	412	4	Q9H5E0	Q9H5E0 homo sapien
29	71	10.9	500	15	Q9IVA4	Q9IVA4 human immu
30	71	10.9	555	4	Q8MB59	Q8MB59 homo sapien
31	70.5	10.9	179	4	Q8RAS3	Q8RAS3 homo sapien
32	70.5	10.9	254	16	Q91024	Q91024 pseudomonas
33	70.5	10.9	348	2	052641	052641 pseudomonas
34	70.5	10.9	348	2	059715	059715 pseudomonas
35	70.5	10.9	348	2	051972	051972 pseudomonas
36	70.5	10.9	402	4	Q96163	Q96163 homo sapien
37	70.5	10.9	449	15	Q999X1	Q999X1 feline immu
38	70.5	10.9	449	15	Q999X2	Q999X2 feline immu
39	70.5	10.9	592	11	Q9JLN5	Q9JLN5 mus musculu
40	70	10.8	112	6	Q9GMM4	Q9GMM4 macaca fasc
41	70	10.8	253	6	Q951B6	Q951B6 ovis aries
42	70	10.8	335	5	Q9TXV5	Q9TXV5 caenorhabdi
43	70	10.8	346	10	Q9ZPT9	Q9ZPT9 arabidopsis
44	70	10.8	389	16	Q8PKX9	Q8PKX9 xanthomonas
45	70	10.8	562	16	Q9K3S5	Q9K3S5 streptomyce

ALIGNMENTS

RESULT 1	ID	Q9DIY3	PRELIMINARY:	PRT:	113 AA.
AC	Q9DIY3	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	A930034P04RIK				
GN	A930034P04RIK				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Retina;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,				
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakel I., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Guistincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,				
RA	Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,				
RA	Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK020928; BAB32259.1;				
DR	MGI; MGI:1925086; A930034P04RIK.				

5Q SEQUENCE 113 AA; 12818 MW; AC01FC9840640E6E/CRC64;

Query Match 64.8%; Score 420.5; DB 11; Length 113;
Best Local Similarity 67.8%; Pred. No. 4.3e-40;
Matches 80; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

OY 1 MPREDARFYGVPRKGGHSHYTAEEAGIGLTVLLIGWYCRRGYBALMDK 60
DB 1 MPOEDIH--GTPRGHRSYTYAEANGNGLVGLIGWYCRRGYBALMDK 58
OY 61 SLHVGTCALRRRCQEGFDRHSKVSLOEKNCSEVPVNPAPYEKLSAQSPPYSP 118
DB 59 RRHIGIKTSRSCSCESPDRHDSRLSQRKSHQVVPVNPAPYEKLS--SPPYSP 113

RESULT 2

014687 ID .014687 PRELIMINARY; PRT; 4957 AA.
AC 014687;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ALR.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97388474; Pubmed=9247308;
RA Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
RA Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
RA Canaan E.;
RT *Structure and expression pattern of human ALR, a novel gene with
RT strong homology to ALR-1 involved in acute leukemia and to Drosophila
RT trithorax.*
RL Oncogene 15:549-560(1997).
CC -1 SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL: AF010404: AAC51735.1;
DR InterPro: IPR003889; Fitch.C.
DR InterPro: IPR003888; Fitch.N.
DR InterPro: IPR000910; HMG_12_box.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR006118; Recombinase.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001965; Znf_PHD.
DR Pfam: PF00628; PHD; 3.
DR SMART: SM00542; FYRC; 1.
DR SMART: SM00541; FYRN; 1.
DR SMART: SM00398; HMG; 1.
DR SMART: SM00249; PHD; 4.
DR SMART: SM00508; PostSET; 1.
DR SMART: SM00317; SET; 1.
DR PROSITE: PS00398; RECOMBINASES_2; 1.
DR PROSITE: PS50280; SET; 1.
DR PROSITE: PS50016; ZF_PHD_2; 1.
SQ SEQUENCE 4957 AA; 531840 MW; 1026562E1419CE8D CRC64;

Query Match 13.4%; Score 87; DB 4; Length 4957;
Best Local Similarity 31.2%; Pred. No. 3.2;
Matches 25; Conservative 7; Mismatches 30; Indels 18; Gaps 3;

OY 41 LLIGCWGRRRNGRYALMDKSLHVGTCALTR---RCPQEGFDRHSKVSLOEKNCSEVP 96
DB 939 LLIGCRHCR-----MMHAGCESLFTEDVDVNAHDEGFD---CVSCOPYVVKPY 984
OY 97 VPNPAPYEKLSAQSPPY 116
DB 985 APVAPPPELVPMKVEPEPY 1004

RESULT 3

014686 ID .014686 PRELIMINARY; PRT; 5262 AA.
AC 014686;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ALR.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97388474; Pubmed=9247308;
RA Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
RA Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
RA Canaan E.;
RT *Structure and expression pattern of human ALR, a novel gene with
RT strong homology to ALR-1 involved in acute leukemia and to Drosophila
RT trithorax.*
RL Oncogene 15:549-560(1997).
CC -1 SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL: AF010403: AAC51734.1;
DR Gene; HGNC:7133; M12.
DR InterPro: IPR003889; Fitch.C.
DR InterPro: IPR003888; Fitch.N.
DR InterPro: IPR000910; HMG_12_box.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR006118; Recombinase.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001965; Znf_PHD.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00628; PHD; 5.
DR SMART: SM00542; FYRC; 1.
DR SMART: SM00541; FYRN; 1.
DR SMART: SM00398; HMG; 1.
DR SMART: SM00249; PHD; 7.
DR SMART: SM00508; PostSET; 1.
DR SMART: SM00184; RING; 3.
DR SMART: SM00317; SET; 1.
DR PROSITE: PS00398; RECOMBINASES_2; 1.
DR PROSITE: PS50280; SET; 1.
DR PROSITE: PS50016; ZF_PHD_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 5262 AA; 564171 MW; 26B7C74CAD417E44 CRC64;

Query Match 13.4%; Score 87; DB 4; Length 5262;
Best Local Similarity 31.2%; Pred. No. 3.5;
Matches 25; Conservative 7; Mismatches 30; Indels 18; Gaps 3;

OY 41 LLIGCWGRRRNGRYALMDKSLHVGTCALTR---RCPQEGFDRHSKVSLOEKNCSEVP 96
DB 1244 LLIGCRHCR-----MMHAGCESLFTEDVDVNAHDEGFD---CVSCOPYVVKPY 1289
OY 97 VPNPAPYEKLSAQSPPY 116
DB 1290 APVAPPPELVPMKVEPEPY 1309

RESULT 4

093NK7 ID .093NK7 PRELIMINARY; PRT; 2034 AA.
AC 093NK7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE AMPK.
GN Streptomyces nodosus.
OS Bacteria; Actinobacteriales; Actinomycetales;


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OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=40318;
RN [1]
RP SEQUENCE FROM N.A.
RA Caffrey P., Lynch S.V., Flood E.M., Finnian S.M., O'Leary M.;
RT "The amphotericin biosynthetic gene cluster from Streptomycetes
   nodosus."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASIS/REDUCTASES
   (SDR) FAMILY.
DR EMBL: AF357202; AAK73503.1;
DR InterPro: IPR001227; Ac_transferase.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR000794; Ketoacyl-synt.
DR InterPro: IPR006163; Pp_bind.
DR InterPro: IPR000379; Ser_estrs_site.
DR InterPro: IPR001031; Thioesterase.
DR Pfam: PF00698; Acyl_transf. 1.
DR Pfam: PF00106; adh_short. 1.
DR Pfam: PF02801; ketoacyl-synt.C; 1.
DR Pfam: PF00550; pp-binding. 1.
DR Pfam: PF00975; Thioesterase; 1.
DR PROSITE: PS50075; ACP_DOMAIN. 1.
DR PROSITE: PS00606; B_KETOACYL_SYNT_HASE; 1.
DR Oxidoreductase; Phosphopantetheine; Transferase.
KM SEQUENCE 2034 AA; 212063 MW; 835962B7DC3D5747 CRC64;

Query Match 12.5%; Score 81; DB 2; Length 2034;
Best Local Similarity 26.8%; Pred. No. 5.6;
Matches 33; Conservative 14; Mismatches 44; Indels 32; Gaps 6;

OY 11 GYPKHGHSYTTAEAGAGIGILTVILGVLILGICWCRNRNGRRLMDKSLHY----- 64
DB 370 GYKVSNGH---TQAAAGAGATKMTAL-----RHG---LLPRLHLDADSTH 412
OY 65 -----GTGCALTRRCPC-QEGFDRHDSKVS---LQEKNCPEVVPNAPPAYEKLSAQSP 115
DB 413 VQMDAGHVSLLTATPWESEGTNRACGVSSFGISGTNAHYTLERAPAEEDTDAEQRP 472
OY 116 YSP 118
DB 473 VVP 475

RESULT 5
O9R201 PRELIMINARY; PRT; 344 AA.
ID O9R201
AC O9R201;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE T-cell surface antigen CD2.
GN CD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/CJ; TISSUE=Spleen;
RA Ma R.2.; Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/CJ; TISSUE=Spleen;
RA Ma R.2.; Cory T.;
RT "CD2 is a candidate gene for Tmewd3 in mice."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF06509; AAD25889.1;
DR EMBL: AF306543; AAG27722.1;
DR HSP: P08921; 1A64.
DR MCD; MGI:88320; Cd2.

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DR InterPro: IPR000719; Prot_Kinase.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
SQ SEQUENCE 344 AA; 38325 MW; 3808BBF9FE2FE3B CRC64;

Query Match 12.4%; Score 80.5; DB 11; Length 344;
Best Local Similarity 27.4%; Pred. No. 0.83;
Matches 31; Conservative 15; Mismatches 46; Indels 21; Gaps 5;

OY 3 REDAHFTGYPKHGHSYTTAEAGAGIGILTVILGVLILGICWCRNRNGRRLMDKSL 62
DB 188 KESKTEVNCPEKGLSF-YTVGVGAG-GLLTVL-VALFIC-ICKRRRRRRRDEEL 243
OY 63 HVGTCALTRRCPCQEGFDRHDSKVS-LQEKNCPEVVPNAPPAYEKLSAQSP 115
DB 244 EI-----KASRTSTVERGPFPHSTPAAAGNVALQHP 279

RESULT 6
O9P571 PRELIMINARY; PRT; 1127 AA.
ID O9P571
AC O9P571;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Related to actin-interacting protein AIP3.
GN B9J10.100.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Algn V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nykatura G., Meves H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL356324; CAB92017.2;
DR InterPro: IPR005613; AIP3.
DR Pfam: PF03915; AIP3; 1.
SQ SEQUENCE 1127 AA; 122731 MW; B6727C2CFB031DDC CRC64;

Query Match 12.4%; Score 80.5; DB 3; Length 1127;
Best Local Similarity 25.6%; Pred. No. 3.2;
Matches 34; Conservative 16; Mismatches 52; Indels 31; Gaps 7;

OY 11 GY-PKKGHSYTTAEAGAGIGILTVILGVLILGICWCR-----RRNGR--ALMDK 61
DB 223 GYGPGRGGRPS-----SSGVPTRTSTYMAVSAGLTMNLEGLSNGTRPDSFRDS 276
OY 62 LHVQ-TGCALTRRCPCQEGFDRHDSKVS-LQEKNCPEVVPNAPPAYEKLSAQSP 105
DB 277 RNSGPTTASPTTRLPSSQDSGVSYSQSSLSSTWMTQNPVMAVPGERTIPGPAP 336
OY 106 KLSAQSPPTSP 118
DB 337 EINVDNFPPTPP 349

RESULT 7
O994J1 PRELIMINARY; PRT; 494 AA.
ID O994J1
AC O994J1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gag protein (gag polypeptide).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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08N504
ID 08N504 PRELIMINARY; PRT; 488 AA.
AC 08N504:
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033132; AAH3132.1; -
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF like.
DR Pfam: PF00200; disintegrin.1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 488 AA; 52722 MW; F9D288B23529BC05 CRC64;
Query Match 11.9%; Score 77; DB 4; Length 488;
Best Local Similarity 25.5%; Pred. No. 3.1; Mismatches 54; Indels 32; Gaps 7;
Matches 35; Conservative 16;
QY 4 EDNAFTGYGYP-----KKGHGSHYTTA---EEAAG---IGILTVILGVLLIGCWYCRNRN 52
DB 238 QNCHCLPGWAPPCNTPGHSGSIDSGMPPEVGPVAVGLVAILVLAIVLMLMYCCRON 297
QY - 53 GYRALMDKSLHVTGCALTR-----CP-----QEGFDRDSKYSIQKNCPEVVPNAP 101
DB 298 NKILQQLKPS-----ALPSKLRQGFSCFPRVSONSGTHANPFLQTPGGRKRYINTP 350
QY 102 PAYEKLSAEQSPPPSP 118
DB 351 ---EILRKPSQPPPPRP 364

RESULT 11
Q8TBUT7
ID 08TBUT7 PRELIMINARY; PRT; 491 AA.
AC 08TBUT7:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024214; AAH24214.1; -
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF like.
DR Pfam: PF00200; disintegrin.1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.

DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 491 AA; 53045 MW; BACD338C38496A08 CRC64;
Query Match 11.9%; Score 77; DB 4; Length 491;
Best Local Similarity 25.5%; Pred. No. 3.1; Mismatches 54; Indels 32; Gaps 7;
Matches 35; Conservative 16;
QY 4 EDNAFTGYGYP-----KKGHGSHYTTA---EEAAG---IGILTVILGVLLIGCWYCRNRN 52
DB 241 QNCHCLPGWAPPCNTPGHSGSIDSGMPPEVGPVAVGLVAILVLAIVLMLMYCCRON 300
QY 53 GYRALMDKSLHVTGCALTR-----CP-----QEGFDRDSKYSIQKNCPEVVPNAP 101
DB 301 NKILQQLKPS-----ALPSKLRQGFSCFPRVSONSGTHANPFLQTPGGRKRYINTP 353
QY 102 PAYEKLSAEQSPPPSP 118
DB 354 ---EILRKPSQPPPPRP 367

RESULT 12
Q9AUC2
ID 09AUC2 PRELIMINARY; PRT; 750 AA.
AC 09AUC2:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Receptor-like protein kinase 1.
GN PRKL
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Kim H.-U., Colter R., McCormick S.;
RT Arabidopsis: the tomato kinases identified in tomato, maize and
RT expression patterns during pollen tube growth."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Dodds P., Kulikauskas R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243041; AAK28346.1; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR007090; LRR_plant.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF000560; LRR; 4.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; kinase; transferase.
KW SEQUENCE 750 AA; 79386 MW; 34B12797F000351B CRC64;
Query Match 11.9%; Score 77; DB 10; Length 750;
Best Local Similarity 24.3%; Pred. No. 5.1; Mismatches 25; Conservative 14; Indels 24; Gaps 3;
QY 14 KKGHGSHYTTAEAAIGILTVILGVLLIGCWY---CRNRNGYRALMDKSLHVTGCALT 71
DB 305 KQEGHAKPYEGSGTSTFGVLAIFIGLIGAVFVALRRRGY-----KTKNGGPTAS-- 357
QY 72 RRCPEGFDRHDSKYSIQKNCPEVVPNAPPAYEKLSAEQSP 114

Db 358 -----SARSPDPPEPPEPPAKKASAAQAPP 385

RESULT 13

ID Q9UKJ1 PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Inhibitory receptor PILRalpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20127940; PubMed-10660620;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRbeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -;
DR InterPro; IPR003599; IG-
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1-like.
DR PROSITE; PS50835; IG_LINK; 1.
KW Receptor.
SQ SEQUENCE 303 AA; 33877 MW; 0410ADFC7E80928B CRC64;

Query Match 11.7%; Score 76; DB 4; Length 303;
Best Local Similarity 20.8%; Pred. No. 2.3;
Matches 25; Conservative 22; Mismatches 39; Indels 34; Gaps 5;

QY 21 YTTAEAGIGILTVILGVL--TGC--WYCRNRNGYRALMDKSLHWGTCALTRCPQ 76
DB 191 HISLETAVGAVAVVAVLGMILGICLRW--RRRKGQR-----TKATTPAREPF 239
QY 77 EGFPHRDSKVSLOENRCEPV-----PNAPEYELSLAQSPPPS 117
DB 240 QNTEPYENIRNEGONTDPKINPKDDGIYVSLALSSYSPAPPSHRLKSPQNETLVS 299

RESULT 14

ID Q9UKJ0 PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Activating receptor PILRbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20127940; PubMed-10660620;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRbeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161081; AAD52965.1; -;
DR InterPro; IPR003599; IG-
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LINK; 1.
KW Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;

Query Match 11.6%; Score 75.5; DB 4; Length 227;
Best Local Similarity 43.8%; Pred. No. 1.9;
Matches 21; Conservative 6; Mismatches 14; Indels 7; Gaps 3;

QY 15 KGHGHSY-----TTAEAGIGIL-TVILGVLILGICWYCRNRNGYRA 56
DB 176 KGHSESMHLSIDPAIRVALAVAVLKTVILGLLILLMW--RRRGSRA 222

RESULT 15

ID Q9J455 PRELIMINARY; PRT; 107 AA.
AC Q9J455;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE Putative fusion protein (Nonstructural protein).
OS Human rotavirus B.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_Taxid=10942;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAL-1;
RA Sen A., Das S., Krishnan T., Kobayashi N., Naik T.N.;
RT "partial sequence of cDNA of the gene segment 6 encoding fusion
protein and a nonstructural protein of the human group B rotavirus
strain, CAL-1.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAL;
RA Kobayashi N., Naik T.;
RT "Sequence of the sixth RNA segment of group B human rotavirus CAL.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF203812; AAF69263.1; -;
DR EMBL; AF230975; AAG09741.1; -;
SQ SEQUENCE 107 AA; 11697 MW; 3AD1596D92B387FE CRC64;

Query Match 11.6%; Score 75; DB 12; Length 107;
Best Local Similarity 38.1%; Pred. No. 0.92;
Matches 16; Conservative 12; Mismatches 8; Indels 6; Gaps 2;
QY 27 AAGIGILTVILGVL--LIGWYCR--RRNGYRALMDKSL 62
DB 42 AAGVGILATLIVLLCSCVINCYLCKRLKRTNGVSSILEENL 83

Search completed: October 7, 2003, 18:49:15
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 18:42:34 ; Search time 11 seconds

(without alignments)
504.468 Million cell updates/sec

Title: US-09-898-860-2
Perfect score: 649
Sequence: 1 MPREDAHFTGYPRKKGHS.....NAPPAYEKLSAEQSPPPYSP 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64.9	100.0	118	MAR1_HUMAN	Q16655 homo sapien
2	80.5	12.4	344	CD2_MOUSE	P08920 mus musculu
3	77	11.9	710	NASC_BACSU	P42434 bacillus su
4	77	11.9	956	AD15_HUMAN	Q9H013 homo sapien
5	72.5	11.2	815	AD15_MOUSE	O88839 mus musculu
6	72.5	11.2	1429	EXPA_DROME	Q07436 drosophila
7	71	10.9	1069	PCHT7_HUMAN	O60245 homo sapien
8	70.5	10.9	202	TMG2_HUMAN	O14669 homo sapien
9	69.5	10.7	218	TMG1_HUMAN	O14668 homo sapien
10	69.5	10.7	401	LSG1_HAEN	P13399 haemophilus
11	68	10.5	188	CYTL_MOUSE	O6v1k7 mus musculu
12	67.5	10.4	188	COME_MERCA	P58416 methanococc
13	67.5	10.4	778	MGDI_HUMAN	Q9Y5V3 homo sapien
14	67.5	10.4	4590	FATH_HUMAN	Q14517 homo sapien
15	66.5	10.2	775	MGDI_MOUSE	Q9YH6 mus musculu
16	66.5	10.2	775	MGDI_MOUSE	O96873 rattus norv
17	66	10.2	140	YD23_YEAST	O07549 saccharomyc
18	66	10.2	969	SACB_STREU	Q55242 streptococc
19	65.5	10.1	258	BOX3_MOUSE	P53771 notophthalm
20	65.5	10.1	659	SYT_THETH	P56881 thermus the
21	65.5	10.1	1436	WC11_BOVIN	P30205 bos taurus
22	65	10.0	356	YHCC_ECOLI	P85045 escherichia
23	65	10.0	356	RS41_ARATH	P92966 arabidopsis
24	64.5	9.9	154	CYTL_HUMAN	Q96J86 homo sapien
25	64.5	9.9	359	FIX2_RHILE	P07748 rhizobium 1
26	64	9.9	144	TIM2_RABIT	O9T877 cyclocolagus
27	64	9.9	344	CD2_RAT	P08921 rattus norv
28	64	9.9	352	CD5L_MOUSE	O66578 mus musculu
29	64	9.9	2180	POIG_EG2H	Q66578 e genome po
30	63.5	9.8	118	VPX_STYAI	O02842 simian immu
31	63.5	9.8	227	NK1L_MOUSE	P27811 mus musculu
32	63.5	9.8	628	GIDA_WIGBR	O8D3K0 wigglewort
33	63.5	9.8	1338	ACIN_MOUSE	O9J1X8 mus musculu

ALIGNMENTS

34	63	9.7	117	1	HYPA_HELPY	O25539 helicobacte
35	63	9.7	336	1	EPB2_MOUSE	P52800 mus musculu
36	63	9.7	387	1	GIR_HUMAN	Q9N183 homo sapien
37	63	9.7	629	1	GIDA_HAEN	P44763 haemophilus
38	63	9.7	1004	1	PHC1_HUMAN	P78364 homo sapien
39	63	9.7	1012	1	PHC1_MOUSE	O64028 mus musculu
40	62.5	9.6	757	1	KNC3_HUMAN	O14803 homo sapien
41	62.5	9.6	786	1	CRJ2_HUMAN	Q9N875 homo sapien
42	62.5	9.6	821	1	ENV_STYGB	P22380 simian immu
43	62.5	9.6	889	1	KNC3_RAT	O01956 rattus norv
44	62.5	9.6	913	1	DDRL_HUMAN	O08345 h epithelia
45	62	9.6	286	1	TESB_HAEN	P44498 haemophilus

RESULT 1

ID	MAR1_HUMAN	STANDARD:	PRT:	118 AA.
AC	Q16655:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Melanoma antigen recognized by T-cells 1 (MART-1) (Melan-A protein)			
DE	(Antigen SK29-AA) (Antigen LB39-AA).			
CN	MLANA OR MART1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RX	MEDLINE=94224770; PubMed=8170938;			
RX	MEDLINE=94224770; PubMed=8170938;			
RA	Kawakami Y., Ellyhu S., Delgado C.H., Robbins P.F., Rivoltini L.,			
RA	Topalian S.L., Miki T., Rosenberg S.A.;			
RT	*Cloning of the gene coding for a shared human melanoma antigen			
RT	recognized by autologous T cells infiltrating into tumor.*;			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:3515-3519(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Straussberg R.L., Felting E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Ditachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carlini P.,			
RA	Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			
RA	Bozak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Falley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	*Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.*;			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

CC -1- TISSUE SPECIFICITY: EXPRESSION IS RESTRICTED TO MELANOMA AND
CC MELANOCYTE CELL LINES AND RETINA.
CC -----
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CC	-----	
DR	EMBL; U06452; AAA19238.1; -	
DR	EMBL; U06654; AAA20389.1; -	
DR	EMBL; BC014423; AAH14423.1; -	
DR	PIR: A55253; A55253.	
DR	GeneW: HGNC:7124; M1ANA.	
DR	MIM; 605513; -	
DR	GO: GO:0005887; C: Integral to plasma membrane; TAS.	
DR	GO: GO:0008222; F: tumor antigen; TAS.	
KW	Antigen; Transmembrane.	
FT	TRANSMEM 27 47	POTENTIAL.
SO	SEQUENCE 118 AA; 13157 MW; B755DFE39CFEB16 CRC64;	

Query Match	100.0%	Score 649	DB 1	Length 118
Best Local Similarity	100.0%	Pred. No. 3	4e-61	
Matches 118	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPREDAFITGYPRKKGHSYTTAEAGIGILVILVIGYLLILICWCRCRRNGRYALMDX	60	
Db	1	MPREDAFITGYPRKKGHSYTTAEAGIGILVILVIGYLLILICWCRCRRNGRYALMDX	60	
QY	61	SLAHGTGCALTLRRCPQEGFDHRDSKVSIOEKNCCEPVVPNAPAYEKISLAESQSPPYSP	118	
Db	61	SLAHGTGCALTLRRCPQEGFDHRDSKVSIOEKNCCEPVVPNAPAYEKISLAESQSPPYSP	118	

RESULT 2			
ID	CD2_MOUSE	STANDARD:	PRT: 344 AA.
AC	P08920; O61394;		
DT	01-NOV-1988 (Rel. 09, Created)		
DT	01-NOV-1988 (Rel. 09, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	T-cell surface antigen CD2 precursor (T-cell surface antigen		
DE	T11/Leu-5) (LFA-2) (LFA-3 receptor).		
GN	CD2.		

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-BIO.A;
RX MEDLINE=87276135; PubMed=2440689;
RA Sewell W.A., Brown M.H., Pink P.J., Kozak C.A., Crumpton M.J.;
RT "The murine homologue of the T lymphocyte CD2 antigen: molecular
cloning, chromosome assignment and cell surface expression".
RL Eur. J. Immunol. 17:1015-1020(1987).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68004738; PubMed=2820751;
 RA Clayton L.K., Sayre P.H., Novotny J., Reinherz E.L.;
 RT "Murine and human T11 (CD2) cDNA sequences suggest a common signal
 RT transduction mechanism."; Eur. J. Immunol. 17:1367-1370(1987).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BA1B/c; TISSUE=liver;
 RX MEDLINE=68144486; PubMed=2894031;
 RA Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;

"Exon-intron organization and sequence comparison of human and murine T11 (CD2) genes.";
Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).

RN [4] SEQUENCE FROM N.A.
 RP MEDLINE=68140313; Pubmed-3257775;
 RX Yagita H., Okumura K., Nakaurchi H.;
 RA "Molecular cloning of the murine homologue of CD2. Homology of the
 RT molecule to its human counterpart T11.";
 RL J. Immunol. 140:1321-1326(1988).
 RN [5]
 RP INTERACTION WITH CD2AP
 RX MEDLINE=98412662; Pubmed-9741631.

CC KA Dustin M., Ulszow M.W., Holdorf A.D., Li J., Bromley S., Desai N.,
CC RA Wilder P., Rosenberger F., van der Merwe P.A., Allen P.M., Shao A.S.,
CC RT "A novel adaptor protein orchestrates receptor patterning and
CC RL cytoskeletal polarity in T-cell contacts." Cell 94:667-677(1998).
CC
CC -I- FUNCTION: CD2 interacts with lymphocyte function-associated
CC antigen (LFA-3) and CD48/BCAM to mediate adhesion between T
CC cells and other cell types. CD2 is implicated in the triggering
CC of T-cells, the cytoplasmic domain is implicated in the
CC signaling function.
CC
CC -I- SUBUNIT: Interacts with CD2AP.
CC
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -I- STRUCTURE: Contains 1 immunoglobulin-like extrinsic domain

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DR EMBL; Y000023; CAA68258.1; -
DR EMBL; Y051423; CAA206500.1; -

DR EMBL, A00145; CAA23500.1; -
DR EMBL, M19607; AAA37393.1; JOINED.
DR EMBL, M19799; AAA37393.1; JOINED.
DR EMBL, M19801; AAA37393.1; JOINED.
DR EMBL, M19803; AAA37393.1; JOINED.
DR EMBL, M19605; AAA37393.1; JOINED.
DR EMBL, M18934; AAA37397.1; -
DR PIR, I49585; I49585.
DR HSSP: P08921; 1A6A.
DR MGD; MGI:88320; Cd2.
DR GO; GO:0005515; F:protein binding activity; ISS.
DR GO; GO:0004872; F:receptor activity; ISS.

DR	PROSITE: PS50835; IG-LIKE: FALSE NEG.
KM	Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
KW	Cell adhesion; Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID

FT	DISOILED	140	180	BY SIMILARITY.
FT	CAROHND	82		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHND	94	94	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHND	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHND	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	99	99	Y -> T (IN REF. 3).
FT	CONFLICT	128	128	M -> V (IN REF. 3 AND 4).
FT	CONFLICT	139	139	T -> I (IN REF. 4).
FT	CONFLICT	175	175	N -> A (IN REF. 3).
FT	CONFLICT	175	175	N -> S (IN REF. 4).
FT	CONFLICT	191	191	K -> N (IN REF. 2).
FT	CONFLICT	192	192	M -> T (IN REF. 3 AND 4).

SQ	SEQUENCE	344	AA;	38414	MM;	CFD12FECBD1444450	CRC64;
Query Match		12.48;	Score 80.5;	DB 1;	Length 344;		

Best Local Similarity 27.4%; Pred. No. 0.44; Matches 31; Conservative 15; Mismatches 46; Indels 21; Gaps 5;

QY 3 REDAHFYGPKRGHSHYTAEEAGIGITVLIGVTLICWCYCRRRNGYRALMDKSL 62
 Db 188 KESMEYVNCPEKLSF-YTVYGAG-GLLVTL-VALFTFC-ICKRRKRRKDEEL 243
 QY 63 HVGTCALTRCPQEGFDRSKVSLQEKNCPEVYPNAPPAEYKLSAOSPP 115
 Db 244 EI-----KASRSTYVERGPKPHSTPAAANQNSVALQAPPP 279

RESULT 3

NASC_BACSU
 ID NASC_BACSU STANDARD; PRT; 710 AA.
 PC P42434;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Asimilatory nitrate reductase catalytic subunit (EC 1.7.99.4).
 GN NASC OR NARB OR NASBB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124189; PubMed=8969502;
 RA Yamae K., Kumano M., Kurita K.,
 RT "The 25 degrees-36 degrees region of the Bacillus subtilis
 RT chromosome: determination of the sequence of a 146 kb segment and
 RT identification of 113 genes.";
 RL Microbiology 142:3047-3056(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bojotin A., Borchert S.,
 RA Boriss R., Boursier L., Bessieres P., Braun M., Brigelli S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denlot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Frits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Katsuma D., Kasahara Y., Klastri-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mosti D., Nakai S., Nodack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Pario V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadleir Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Solido B.,
 RA Sorokin A., Taccoti E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni K.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanter F., Vassart A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamae K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 35-710 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=9513124; PubMed=7866621;
 RA Ogawa K.-I., Akaigawa E., Yamae K., Sun Z.-W., Lancelle M., Zuber P.,

RA Nakano M.M.;
 RT "The nasB operon and nasB gene are required for nitrate/nitrite
 RT assimilation in Bacillus subtilis.";
 RL J. Bacteriol. 177:1409-1413(1995).
 CC -1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
 CC STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
 CC -1- CATALYTIC ACTIVITY: Nitrite + acceptor -> nitrate + reduced
 CC acceptor.
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
 CC -1- PATHWAY: Nitrate assimilation (denitrification).
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY.
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 CC -----
 CC DR EMBL; D50453; BAA08965.1; -
 CC DR EMBL; Z99105; CAB12125.1; -
 CC DR EMBL; D30689; BAA06353.1; -
 CC DR PIR; E69665; E69665.
 CC DR HSSP; P81186; 2NAP.
 CC DR Subtilist; BG11095; nasC.
 CC DR InterPro; IPR006657; Mol_dinuc_bind.
 CC DR InterPro; IPR006963; Molybdop_Fe4S4.
 CC DR InterPro; IPR006656; Molybdopterin.
 CC DR InterPro; IPR006655; Prok_Moxred.
 CC DR Pfam; PF04879; Molybdop_Fe4S4; 1.
 CC DR Pfam; PF00384; molybdopterin; 1.
 CC DR Pfam; PF01568; Molybdop_binding; 1.
 CC DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
 CC DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
 CC DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; FALSE NEG.
 CC DR Oxidoreductase; Molybdenum; Nitrate assimilation; Iron-sulfur; 4Fe-4S;
 CC KW Complete proteome.
 CC FT METAL 26 26 IRON-SULFUR (4FE-4S) (POTENTIAL).
 CC FT METAL 29 29 IRON-SULFUR (4FE-4S) (POTENTIAL).
 CC FT METAL 33 33 IRON-SULFUR (4FE-4S) (POTENTIAL).
 CC FT METAL 63 63 IRON-SULFUR (4FE-4S) (POTENTIAL).
 CC SQ SEQUENCE 710 AA; 78575 MW; 625E8664A1552AA2 CR664;
 CC -----
 CC Query Match 11.9%; Score 77; DB 1; Length 710;
 CC Best Local Similarity 32.4%; Pred. No. 2.2;
 CC Matches 34; Conservative 8; Mismatches 37; Indels 26; Gaps 6;
 QY 15 KGHGSHYTAEE-----AAGIGITVLIGVTLIGCWT--CRRNGYRALMDKSLNVT 66
 Db 507 KGRFYSYSAEDIFENELREASRG-----GIADYSGISYGRLRGGIHMPCPSDHPGT 560
 QY 67 QCATLRCPQEGFDRSKVSLQEKNCPEVYPNAPPA-YEKLSAE 110
 Db 561 GRLLT-----ESFNPDPKALSL-----VIPNEPVRKEKRTAD 594
 RESULT 4
 AD19_HUMAN
 ID AD19_HUMAN STANDARD; PRT; 956 AA.
 AC Q9H013; Q9BZL5; Q9UHP2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE ADAM 19 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE domain 19) (Mellitin beta) (Metalloprotease and disintegrin dentritic
 DE antigen marker) (MADAM).
 GN ADAM19 OR MLTNB OR PRSG34.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;

Query Match	Best Local Similarity	Matches	Score	DB 1	Length	956	DB 2	Length	956	DB 3	Length	956	DB 4	Length	956	DB 5	Length	956	DB 6	Length	956	DB 7	Length	956	DB 8	Length	956	DB 9	Length	956	DB 10	Length	956	DB 11	Length	956	DB 12	Length	956	DB 13	Length	956	DB 14	Length	956	DB 15	Length	956	DB 16	Length	956	DB 17	Length	956	DB 18	Length	956	DB 19	Length	956	DB 20	Length	956	DB 21	Length	956	DB 22	Length	956	DB 23	Length	956	DB 24	Length	956	DB 25	Length	956	DB 26	Length	956	DB 27	Length	956	DB 28	Length	956	DB 29	Length	956	DB 30	Length	956	DB 31	Length	956	DB 32	Length	956	DB 33	Length	956	DB 34	Length	956	DB 35	Length	956	DB 36	Length	956	DB 37	Length	956	DB 38	Length	956	DB 39	Length	956	DB 40	Length	956	DB 41	Length	956	DB 42	Length	956	DB 43	Length	956	DB 44	Length	956	DB 45	Length	956	DB 46	Length	956	DB 47	Length	956	DB 48	Length	956	DB 49	Length	956	DB 50	Length	956	DB 51	Length	956	DB 52	Length	956	DB 53	Length	956	DB 54	Length	956	DB 55	Length	956	DB 56	Length	956	DB 57	Length	956	DB 58	Length	956	DB 59	Length	956	DB 60	Length	956	DB 61	Length	956	DB 62	Length	956	DB 63	Length	956	DB 64	Length	956	DB 65	Length	956	DB 66	Length	956	DB 67	Length	956	DB 68	Length	956	DB 69	Length	956	DB 70	Length	956	DB 71	Length	956	DB 72	Length	956	DB 73	Length	956	DB 74	Length	956	DB 75	Length	956	DB 76	Length	956	DB 77	Length	956	DB 78	Length	956	DB 79	Length	956	DB 80	Length	956	DB 81	Length	956	DB 82	Length	956	DB 83	Length	956	DB 84	Length	956	DB 85	Length	956	DB 86	Length	956	DB 87	Length	956	DB 88	Length	956	DB 89	Length	956	DB 90	Length	956	DB 91	Length	956	DB 92	Length	956	DB 93	Length	956	DB 94	Length	956	DB 95	Length	956	DB 96	Length	956	DB 97	Length	956	DB 98	Length	956	DB 99	Length	956	DB 100	Length	956	DB 101	Length	956	DB 102	Length	956	DB 103	Length	956	DB 104	Length	956	DB 105	Length	956	DB 106	Length	956	DB 107	Length	956	DB 108	Length	956	DB 109	Length	956	DB 110	Length	956	DB 111	Length	956	DB 112	Length	956	DB 113	Length	956	DB 114	Length	956	DB 115	Length	956	DB 116	Length	956	DB 117	Length	956	DB 118	Length	956	DB 119	Length	956	DB 120	Length	956	DB 121	Length	956	DB 122	Length	956	DB 123	Length	956	DB 124	Length	956	DB 125	Length	956	DB 126	Length	956	DB 127	Length	956	DB 128	Length	956	DB 129	Length	956	DB 130	Length	956	DB 131	Length	956	DB 132	Length	956	DB 133	Length	956	DB 134	Length	956	DB 135	Length	956	DB 136	Length	956	DB 137	Length	956	DB 138	Length	956	DB 139	Length	956	DB 140	Length	956	DB 141	Length	956	DB 142	Length	956	DB 143	Length	956	DB 144	Length	956	DB 145	Length	956	DB 146	Length	956	DB 147	Length	956	DB 148	Length	956	DB 149	Length	956	DB 150	Length	956	DB 151	Length	956	DB 152	Length	956	DB 153	Length	956	DB 154	Length	956	DB 155	Length	956	DB 156	Length	956	DB 157	Length	956	DB 158	Length	956	DB 159	Length	956	DB 160	Length	956	DB 161	Length	956	DB 162	Length	956	DB 163	Length	956	DB 164	Length	956	DB 165	Length	956	DB 166	Length	956	DB 167	Length	956	DB 168	Length	956	DB 169	Length	956	DB 170	Length	956	DB 171	Length	956	DB 172	Length	956	DB 173	Length	956	DB 174	
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SQ SEQUENCE 815 AA; 87424 MW; C064BD3B7347D19B CRC64;
 Query Match 11.2%; Score 72.5; DB 1; Length 815;
 Best Local Similarity 20.9%; Pred. No. 7.7;
 Matches 28; Conservative 17; Mismatches 40; Indels 49; Gaps 5;

QY 14 KKGHGHVY-----TTAEAGIGILTVILGVLILGICWYCR 50
 DB 660 KKGHGHVYCCSSGRCCEBGNAPPDCKMTQKATSSITGTLISLLLVLLGASTYHR 719
 QY 51 RRGYRALMDKSLHVTGOCALTRRCPOBGFDRHDSKVSLSQEKNCBPVPNPAPAYEKLSAE 110
 DB 720 ARLEHQRILCQLK--GSSCQY--RAPQ-----SCPPERGPFOBAQOMGT 759
 QY 111 QS-----PPPYSP 118
 DB 760 KSGGPRKPPPPRKP 773

RESULT 6
 EXPLDROME STANDARD; PRT: 1429 AA.
 AC Q07436;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Expanded protein.
 GN Ex.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Imaginal disks;
 RX MEDLINE=94094747; PubMed=8269855;
 RA Boedihelmer M., Laugheon A.;
 RT "Expanded: a gene involved in the control of cell proliferation in
 RL Imaginal discs.";
 RL Development 118:1291-1301(1993).
 RN [2]
 RP REVISIONS.
 RA Boedihelmer M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE CONTROL OF CELL PROLIFERATION IN
 CC IMAGINAL DISCS. MAY BIND TO CERTAIN PROTEINS OF SIGNAL
 CC TRANSDUCTION PATHWAYS BY INTERACTION WITH THEIR SH3 DOMAINS.
 CC -1- SUBCELLULAR LOCATION: APICAL SURFACE OF DISC CELLS.
 CC -1- DISEASE: MUTATIONS OF EXPANDED PROTEIN CAUSE HYPERPLASIA OF THE
 CC IMAGINAL DISC RESULTING IN WING OVERGROWTH. THIS OVERGROWTH IS
 CC LIMITED TO SPECIFIC REGIONS ALONG THE 2 WING AXES. DEFECTS ALSO
 CC IN EYES, HEAD, THORAX AND LIMBS WHERE DUPLICATION AND BULGING
 CC OFTEN OCCUR.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: L14768; AAB3974.1; -
 DR PIR: T13720; T13720.
 DR FLYBASE: FBgn0004583; ex.
 DR InterPro: IPR000299; Band.4.1.
 DR Pfam: PF00373; Band.41; 1.
 DR SMART: SM00295; B41; 1.
 DR PROSITE: PS00660; FERM_1; FALSE_NEG.
 DR PROSITE: PS00661; FERM_2; FALSE_NEG.
 DR PROSITE: PS50057; FERM_3; 1.

KM Developmental protein; SH3-binding.
 FT DOMAIN 26 399 FERM.
 FT SITE 1008 1016 SH3-BINDING (POTENTIAL).
 FT SITE 1012 1020 SH3-BINDING (POTENTIAL).
 FT SITE 1149 1157 SH3-BINDING (POTENTIAL).
 FT DOMAIN 782 788 POLY-GLU.
 FT DOMAIN 952 955 POLY-PRO.
 FT DOMAIN 1002 1005 POLY-HIS.
 FT DOMAIN 1011 1017 POLY-PRO.
 FT DOMAIN 1081 1084 POLY-PRO.
 FT DOMAIN 1149 1154 POLY-PRO.
 FT DOMAIN 1158 1168 POLY-ALA.
 FT DOMAIN 1170 1174 POLY-SER.
 FT DOMAIN 1199 1205 POLY-PRO.
 FT DOMAIN 1416 1424 POLY-GLN.
 SQ SEQUENCE 1429 AA; 153886 MW; 3CB08D2FC4862062 CRC64;

Query Match 11.2%; Score 72.5; DB 1; Length 1429;
 Best Local Similarity 23.4%; Pred. No. 14;
 Matches 37; Conservative 10; Mismatches 52; Indels 59; Gaps 7;

QY 2 PREDARFTYGYPRKKGH-----HSYTAERAGIGILTVILGVLILGICWYCR 54
 DB 708 PRSDNVSTGSSFRDGDSPDTNKHSLSAEFLTN-----LIYG-----RGTY 750
 QY 55 --RALMDKSLH-----VTGOCALTRRCPOBGFDRHDSKVSLSL----- 88
 DB 751 PSRKTVSSSLHSDCDYVTLPLDQGEEDVDPAPPAPPYSAHEKYGICGPPYAKPIPKP 810
 QY 89 -----QEKNCBPVPNPAP-PAYEKLAAESPPYYS 117
 DB 811 IAVVAPKPDSPPCSPVPVPAIPAPPAIRRRDPPYYS 848

RESULT 7
 PCH7_HUMAN STANDARD; PRT: 1069 AA.
 ID PCH7_HUMAN
 AC 060245; 060245; 060247;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protocadherin 7 precursor (Brain-heart protocadherin) (BH-Pcdh).
 GN PCDH7 OR BHPCH7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX MEDLINE=98277460; PubMed=9615233;
 RA Yoshida K., Yoshitomo-Nakagawa K., Seki N., Sasaki M., Sugano S.;
 RT "Cloning, expression analysis, and chromosomal localization of
 RT BH-protocadherin (PCDH7), a novel member of the cadherin
 RT superfamily.";
 RL Genomics 49:458-461(1998).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-3;
 CC Name-A: Synonyms-BH-Pcdh-a;
 CC IsoId=060245-1; Sequence-Displayed;
 CC Name-B: Synonyms-BH-Pcdh-b;
 CC IsoId=060245-2; Sequence-VSP_000704;
 CC Name-C: Synonyms-BH-Pcdh-c; Sequence-VSP_000705; VSP_000706;
 CC IsoId=060245-3; Sequence-VSP_000705; VSP_000706;
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in brain and heart and
 CC at lower levels in various other tissues.
 CC -1- SIMILARITY: Contains 7 cadherin domains.
 CC -----
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DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxylglutamic acid protein 1 precursor (Proline-rich
 DE rich Glu protein 1) (Proline-rich gamma-carboxylglutamic acid protein
 DE 1)
 GN PRKGL OR TWGL OR PRGL.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97404347; PubMed-9256434;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Dave E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 RT gamma-carboxylglutamic acid proteins."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- PTM: Glu residues are produced after subsequent posttranslational
 CC modifications of glutamic acid by a vitamin K-dependent gamma-
 CC carboxylase.
 CC -----
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 CC -----
 CC EMBL: AF009242; AAB67070.1; -
 CC DR HSSP; P00740; ICFH.
 CC DR GeneW; HGNC:9469; PRKGL.
 CC DR MIM: 604428; -
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC DR InterPro; IPR002383; GLA_blood.
 CC DR InterPro; IPR000294; Vitk_dep_GLA.
 CC DR Pfam; PF00594; gla; 1.
 CC DR PRINTS; PR00001; GLABLOOD.
 CC DR SMART; SM00069; GLA; 1.
 CC DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 CC DR Gamma-carboxylglutamic acid; Vitamin K; Transmembrane.
 CC FT PROPEP 1 20
 CC FT CHAIN 1 218
 CC FT TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 CC FT PROTEIN 1.
 CC FT DOMAIN 21 83 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 84 106 POTENTIAL.
 CC FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 24 61 GLA-RICH.
 CC FT DOMAIN 131 135 POLY-PRO.
 CC FT SEQUENCE 218 AA; 24947 MW; 26538A61A80AEB98 CRC64;
 SQ
 Query Match 10.7%; Score 69.5; DB 1; Length 218;
 Best Local Similarity 27.0%; Pred. No. 3.9;
 Matches 30; Conservative 9; Mismatches 37; Indels 35; Gaps 5;
 OY 33 LTVIIGVLLIGCWCRNGRYALMDKSLHVGTCALT-----RRCPOGEFDH----- 81
 DB 91 LFIILIVYILT--WRCFILANKTRRQIVTSGHIPFPHALNITPPPPDEYFSSGSLSPGR 148
 OY 82 -----RDSKVSILQKNCPEVVPNAPAYEKLSAEGS-----PPP 115
 DB 149 LQYVGRSDSVSTRLSNCDP-----PPTYEATGQVNLQRSETEPHLDPPP 194
 RESULT 10
 LSGL_HAEIN STANDARD; PRT; 401 AA.
 AC P71399; Q48210;
 ID 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Isg locus putative protein 1.
 GN H11700.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 NC NCBL_TaxID-727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SYRAIN-A2;
 RA McLaughlin R., Abu Kwaik Y., Young R., Splinola S., Apicella M.;
 RT "Characterization and sequence of the Isg locus from Haemophilus
 RT influenzae."
 RT Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SYRAIN-Rd / KW20 / ATCC 51907;
 RA MEDLINE-9530650; PubMed-7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kervage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Sudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghegan N.S.M.,
 RA Gehler C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RA Rd."
 RA Science 269:496-512(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the polysaccharide synthase family.
 CC H10867/H11700 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M94855; AAA24978.1; -
 CC DR EMBL; U32842; AAC23346.1; ALT_INIT.
 CC DR PIR; H64175; H64175.
 CC DR TIGR; H11700; -
 CC DR InterPro; IPR002797; Polysacc_synt.
 CC DR Pfam; PF01943; Polysacc_synt; 1.
 CC DR Hypothetical protein; Transmembrane; Complete proteome.
 CC FT TRANSMEM 8 28
 CC FT TRANSMEM 36 56
 CC FT TRANSMEM 87 107
 CC FT TRANSMEM 132 152
 CC FT TRANSMEM 162 182
 CC FT TRANSMEM 199 219
 CC FT TRANSMEM 237 257
 CC FT TRANSMEM 282 302
 CC FT TRANSMEM 320 340
 CC FT TRANSMEM 352 372
 CC FT TRANSMEM 374 394
 CC FT TRANSMEM 249 269
 CC FT TRANSMEM 276 296
 CC FT TRANSMEM 358 378
 CC FT TRANSMEM 401 AA; 45944 MW; FE2E7B0274780874 CRC64;
 SQ
 Query Match 10.7%; Score 69.5; DB 1; Length 401;
 Best Local Similarity 21.6%; Pred. No. 7.5;
 Matches 21; Conservative 20; Mismatches 23; Indels 33; Gaps 4;
 OY 6 AHFIYGPKR-----GHGSHYTAEEAAGIGITVLIGVLLIGCW-----YGRRR 51
 DB 63 SRFFYFGKRSIMNVYVGTAYIT-----IIGSTIILIGCWTAQSEILFYALS 110
 OY 52 NGYRALMDKSLHVGTCALTRRCPOGEFDRHDSKVS 88

Db 111 SIFOSFLNVLSTV-----RQCCKKMSYAFIOFSL 140

RESULT 11
CYTL_MOUSE STANDARD: PRT; 165 AA.

AC 08V1H7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine and tyrosine-rich protein 1 precursor (Proline-rich domain containing protein).
GN CYR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Brain;
RX MEDLINE=22057895; PubMed=12062809;
RA Vitale L., Casadei R., Canaider S., Lenzi L., Strippoli P., D'Addabbo P., Giannone S., Carinci P., Zannotti M.;
RT "Cysteine and tyrosine-rich 1 (CYR1), a novel unpredicted gene on human chromosome 21 (21q21.2), encodes a cysteine and tyrosine-rich protein and defines a new family of highly conserved vertebrate specific genes.";
RL Gene 290:141-151(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22032984; PubMed=12036297;
RA Raymond A., Camargo A.A., Deutsch S., Stevenson B.J., Parmigiani R.B., Ucla C., Bettont F., Kossler C., Lyle R., Guilponti M., de Souza S., Iseli C., Jongeneel C.V., Bucher P., Simpson A.J.G., Antonarakis S.E.;
RT "Nineteen additional unpredicted transcripts from human chromosome 21.";
RL Genomics 79:824-832(2002).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC

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CC

CC EMBL: AF442733; AAL35295.1;
DR EMBL: AY061854; AAL35738.1;
DR MGD: MGI:2152187; Cyrl.
KW Signal; Transmembrane.

FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 165 CYSTEINE AND TYROSINE-RICH PROTEIN 1.
FT DOMAIN 30 61 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 62 82 POTENTIAL.
FT DOMAIN 83 165 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 144 149 POLY-PRO.
FT CONFLICT 36 36 R -> H (IN REF. 2).
SO SEQUENCE 165 AA; 18063 MM; 94940DAAE2BCFDC1 CRC64;

Query Match 10.5%; Score 68; DB 1; Length 165;
Best Local Similarity 21.2%; Pred. No. 4.2;
Matches 22; Conservative 19; Mismatches 37; Indels 26; Gaps 5;

QY 28 AGIGILVITGVLIG-----CMYCRRRNGYALMDKSLHVGQCALTRCPQEG 78
DB 59 SGRALAGIVGIVFIMVINGIALICICMCKNNRGTGRGVRAAHINA-ISTPMAPPYT 117
QY 79 FDRH-DSKVSIOEKNCPEVVPNAPAYE---KLSAESPPPYSP 118
DB 118 YDHEMEYRTDL-----PPYSANPQASAGQSPPPYP 149

RESULT 12
COME_METUA STANDARD: PRT; 188 AA.

AC P58416; Q57704;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sulfolpyruvate decarboxylase subunit beta (EC 4.1.1.79).
GN COME OR MJ0256.
OS Methanococcus jannaschli.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hirst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschli.";
RL Science 273:1058-1073(1996).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20398170; PubMed=10940029;
RA Graupner M., Xu H., White R.H.;
RT "Identification of the gene encoding sulfolpyruvate decarboxylase, an enzyme involved in biosynthesis of coenzyme M.";
RL J. Bacteriol. 182:4862-4867(2000).

CC -1- FUNCTION: Catalyzes the decarboxylation of sulfolpyruvic acid to sulfoacetaldehyde.
CC

CC -1- CATALYTIC ACTIVITY: 3-sulfolpyruvate -> 2-sulfoacetaldehyde + CO(2).
CC

CC -1- COFACTOR: TPP (Potential).
CC

CC -1- PATHWAY: Coenzyme M biosynthesis; fourth step.
CC

CC -1- SUBUNIT: Heterododecamer composed of 6 subunits alpha and 6 subunits beta.
CC

CC -1- MISCELLANEOUS: Inactivated by oxygen when heated in air at 80 degrees Celsius.
CC

CC -1- SIMILARITY: BELONGS TO THE TPP ENZYME FAMILY.
CC

CC -1- CAUTION: The sequence corresponding to this entry was originally entered in SWISS-PROT as AC Q57704 in November 1997 and was deleted in July 1999 because TIGR removed the CDS for that ORF. We have recreated it because of the evidence (ref.2) that it really exists.
CC

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CC

CC EMBL: U67480; NOT ANNOTATED_CDS.
DR PIR: A64332; A64332.
DR TIGR: MJ0256;
DR InterPro: IPR000399; Pyruvate decarb.
DR Pfam: PF02775; TPP_enzymes.C.1.
DR PROSITE: PS00187; TPP_ENZYMES; FALSE NEG.
KW Coenzyme M biosynthesis; Lyase; Decarboxylase; Thiamine pyrophosphate; complete proteome.

SO SEQUENCE 188 AA; 20980 MM; 52A6C91E2D43B97D CRC64;
Query Match 10.4%; Score 67.5; DB 1; Length 188;
Best Local Similarity 24.8%; Pred. No. 5.4;

	Matches	26; Conservative	13; Mismatches	45; Indels	21; Gaps	3;
Oy	29	GIGILYIIVLIIIGCMYCRRNGALNMDK-----LHNGQCALTRRCPDGF	79			
		::::: ::: ::: :::				
Dd	72	GDGSIINLSGLSTIG--YMKPKYLIIVIDNSAGTSGNQKHGRKTNELEIAKGGL	129			
Oy	80	D-----HRDSKYSLOEKNEPVVPNPAPYEAKISADSP	114			
		::: ::: ::: :::				
Dd	130	DTITTESIEFEKEFNALNEKKVLAIIATPIINEKSSNIETIP	174			

AC 090YH6; 090PB5; 09CYX1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Melanoma-associated antigen DI (MAGE-DI antigen) (Neurotrophin
 DE receptor-interacting MAGE homolog) (Dlx1n-1).
 GN MAGE-DI OR NRAGE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL:taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE-21265065; PubMed-11084035;
 RA Masuda Y., Sasaki A., Shibuya H., Ueno N., Ikeda K., Watanabe K.;
 RT Dlx1n-1, a novel protein that binds Dlx5 and regulates its
 RT transcriptional function.";
 RL J. Biol. Chem. 276:5331-5338(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Auguter P.H., Chomez P.M., De Backer O.R., Bertrand M.J.M.;
 RT "Ten new murine members of the MAGE gene family.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Glassl C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT *Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 CC -1- FUNCTION: Involved in the apoptotic response after nerve growth
 CC factor (NGF) binding in neuronal cells. Binds p75NTR and
 CC antagonizes its association with TrkA, inhibits cell cycle
 CC progression, and facilitates p75NTR-mediated apoptosis. May act as
 CC a regulator of the function of Dlx family members (By similarity).
 CC -1- SUBUNIT: INTERACTS WITH Dlx5, Dlx7 AND MSX2 AND FORMS
 CC HOMOMULTIMERS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Expression shifts from the
 CC cytoplasm to the plasma membrane upon stimulation with NGF (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in many adult tissues,
 CC except for the spleen. Expressed in osteoblastic and
 CC chondrogenic cell lines and also during embryonic development.
 CC -1- SIMILARITY: Contains 1 MAGE domain.
 CC -----
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 CC -----
 CC DR EMBL; AB029448; BAA87959.1; -;
 CC DR EMBL; AF319975; AAK01203.1; -;

DR EMBL; AK017275; BAB30666.1; -;
 DR EMBL; AK013231; -; NOT_ANNOTATED_CDS.
 DR MGD; MGI:1930187; Maged1.
 DR GO; GO:0005515; F:protein binding activity; IPI.
 DR GO; GO:0003713; F:transcription co-activator activity; IDA.
 DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IDA.
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 KW Antigen; Multigene family; Repeat.
 FT DOMAIN 292 441
 FT
 FT REPEAT 292 297
 FT REPEAT 298 303
 FT REPEAT 304 309
 FT REPEAT 329 334
 FT REPEAT 335 340
 FT REPEAT 341 346
 FT REPEAT 347 352
 FT REPEAT 353 358
 FT REPEAT 359 364
 FT REPEAT 365 370
 FT REPEAT 371 376
 FT REPEAT 377 382
 FT REPEAT 383 388
 FT REPEAT 389 394
 FT REPEAT 395 400
 FT REPEAT 401 406
 FT REPEAT 407 412
 FT REPEAT 413 418
 FT REPEAT 419 424
 FT REPEAT 425 429
 FT REPEAT 430 435
 FT REPEAT 436 441
 FT REPEAT 468 666
 FT DOMAIN 357 662
 FT
 FT CONFLICT 357 662 MISSING (IN REF. 2).
 SQ SEQUENCE 775 AA; 85669 MW; 224B82470816835A CRC64;
 Query Match 10.2%; Score 66.5; DB 1; Length 775;
 Best Local Similarity 28.8%; Pred. No. 31;
 Matches 32; Conservative 11; Mismatches 33; Indels 35; Gaps 6;
 QY 19 HSY---TTAEBAAGI-----GIIVTIVGLILIG-----CWYCRRRNGYRALM 58
 DB 533 HLYVLISTPESLNGILGTTKDTPTGLILVILGIIFPNNGNATVAVFEMLRKGLRGCV 592.
 QY 59 DKSILVGTQCALRR-CPQSGFDHRDSKVSLSQENCEPVVPA-PPAYEKL 107
 DB 593 RHPILGDLRKILTYEFVKOKYIDYRR-----VNSNPPEYEF 630
 Search completed: October 7, 2003, 18:48:34
 Job time : 13 secs